

GenCore version 5.1.6
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leic search, using sw model

February 29, 2004, 19:44:23 ; Search time 10058.5 Seconds
(without alignments)
17262.293 Million cell updates/sec

US-09-424-686F-9

1 gtttcaggcagctgcgtc.....aaaaaaaaaaaaaaaaaaaa 4006

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

3470272 seqs, 21671516995 residues

hits satisfying chosen parameters: 6940544

length: 0
length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_vt.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_man.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Descript
1	3960	98.9	4042	6	AX001446	AX001446
2	3960	98.9	4042	6	AX003121	AX003121
3	3960	98.9	4042	6	BD136185	BD136185
4	3946.6	98.5	4037	6	E36819	E36819 H
5	3946.6	98.5	4037	6	AR390496	AR390496
6	3946.6	98.5	4037	6	AR393110	AR393110
7	3946.6	98.5	4037	6	AX810378	AX810378
8	3946.6	98.5	4037	6	BD011070	BD011070
9	3933.4	98.2	4070	6	AX391846	AX391846
10	3933	98.2	4015	6	AR104587	AR104587
11	3933	98.2	4015	6	AR175848	AR175848
12	3933	98.2	4015	6	E36793	E36793 H
13	3933	98.2	4015	6	AR182221	AR182221
14	3933	98.2	4015	6	AR224455	AR224455
15	3933	98.2	4015	6	AR226390	AR226390
16	3933	98.2	4015	6	AR243328	AR243328
17	3933	98.2	4015	6	AR263555	AR263555
18	3933	98.2	4015	6	AR265996	AR265996
19	3933	98.2	4015	6	AR390470	AR390470
20	3933	98.2	4015	6	AR393084	AR393084
21	3933	98.2	4015	6	AR404030	AR404030
22	3933	98.2	4015	6	AX019310	AX019310
23	3933	98.2	4015	6	AX133979	AX133979
24	3933	98.2	4015	6	AX552695	AX552695
25	3933	98.2	4015	6	AX810036	AX810036
26	3933	98.2	4015	6	BD011044	BD011044
27	3933	98.2	4015	6	BD015832	BD015832
28	3933	98.2	4015	6	BD082985	BD082985
29	3933	98.2	4015	6	BD131727	BD131727
30	3933	98.2	4015	6	BD218834	BD218834
31	3933	98.2	4015	9	AF015950	AF015950
32	3931	98.1	4027	6	BD233924	BD233924
33	3931	98.1	4027	9	AF018167	AF018167
34	3910	97.6	3918	6	BD196293	BD196293
35	3878.8	96.8	3964	6	BD196267	BD196267
36	3796	94.8	4022	6	BD196302	BD196302
37	3786.2	94.5	4029	6	AR104586	AR104586
38	3786.2	94.5	4029	6	AR175847	AR175847
39	3786.2	94.5	4029	6	E36818	E36818 H
40	3786.2	94.5	4029	6	AR390495	AR390495
41	3786.2	94.5	4029	6	AR393109	AR393109
42	3786.2	94.5	4029	6	AX810327	AX810327
43	3786.2	94.5	4029	6	BD011069	BD011069
44	3579	89.3	3855	6	E36795	E36795 H
45	3579	89.3	3855	6	AR243330	AR243330

ALIGNMENTS

RESULT 1	AX001446	AX001446	4042 bp	DNA	linear	PAT
LOCUS	AX001446	Sequence 1 from Patent WO9859040.				
DEFINITION	AX001446	Sequence 1 from Patent WO9859040.				
ACCESSION	AX001446	Sequence 1 from Patent WO9859040.				
VERSION	AX001446.1	GI:7241612				
KEYWORDS	AX001446.1	GI:7241612				
SOURCE	AX001446.1	GI:7241612				
ORGANISM	AX001446.1	GI:7241612				
REFERENCE	AX001446.1	GI:7241612				
AUTHORS	AX001446.1	GI:7241612				
TITLE	AX001446.1	GI:7241612				
JOURNAL	AX001446.1	GI:7241612				

Patent: WO 9859040-A 1 30-DEC-1998;

98.9%;	Score 3960;	DB 6;	Length 4042;	
ilarity 99.1%;	Prod. No. 0;			
Conservative	0;	Mismatches	0;	Indels 36; Gaps 1;
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ATGCGCGCGCTCCCGCTGCGAGCCGTCGCTCCCTGTCTGCGACGCACTACGCGG	120			
GTGTGCGCGCTGGCGACGTTCTGTGCGGCGCTTGGGGCCCCAGGGCTGGCGGCTGTGTGC	180			
GTGTGCGCGCTGGCGACGTTCTGTGCGGCGCTTGGGGCCCCAGGGCTGGCGGCTGTGTGC	180			
CGCGGGAGACCGGGGCGCTTTCGCGCGCTGTGTGGCCCCAGTGCTGTGTGTGTGTGCCTT	240			
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AGACGACGCGCGCCCGCGCGCCCTTCTTCGCGCAGGTGTCTCTGCTGAGAGGAGC	300			
GTGGCCGAGTGTGTGACGAGGCTGTGCGAGCGCGCGCGAGAGACGTGTGTGGGCTTTCG	360			
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TGCCACTCAGGCCCCCGCCCGCACGCTAGTGGACCCCGAAGGCGTCTGGGATGCG	660			
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[illegible]

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Qy	3085	CATTTCATCAGCAAGTTTGGAGAAGACCCCAATTMTTCTCGCGGTCAATCTCTC
Db	3121	CATTTCATCAGCAAGTTTGGAGAAGACCCCAATTMTTCTCGCGGTCAATCTCTC
Qy	3145	CCTCCCTCTGCTACTCCATCCTGAAAGCCCAAGAACGCAGAGGATGTGCTCGGGG
Db	3181	CCTCCCTCTGCTACTCCATCCTGAAAGCCCAAGAACGCAGAGGATGTGCTCGGGG
Qy	3205	GCGCGCGCGGCCCTCTGCCCTCCGAGGCCGTGAGTGGCTGTGCCACCAAGACA
Db	3241	GCGCGCGCGGCCCTCTGCCCTCCGAGGCCGTGAGTGGCTGTGCCACCAAGACA
Qy	3265	TCAAGCTGACTCGACACCGTGTCACTTACGTGCCACTCTCTGGGTCTACTCAGGG
Db	3301	TCAAGCTGACTCGACACCGTGTCACTTACGTGCCACTCTCTGGGTCTACTCAGGG
Qy	3325	AGACGCAGCTGAGTCGGAGCTCCCGGGGACGACGCTGACTGCCCTCGAGGCC
Db	3361	AGACGCAGCTGAGTCGGAGCTCCCGGGGACGACGCTGACTGCCCTCGAGGCC
Qy	3385	ACCGGGCACTGCCCTCAGACTTCAAGACCACTCTCGACTGATGGCCACCCGCC
Db	3421	ACCGGGCACTGCCCTCAGACTTCAAGACCACTCTCGACTGATGGCCACCCGCC
Qy	3445	AGGCCGAGAGCAGACACGAGAGCCCTGTCAAGCCGGCTCTACGTCCCGAGGG
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Qy	3505	GGCGGCCACACCAAGGCCCGCAGCGCTGGGAGTCTGAGGCGCTCAGGTGAGTGT
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Qy	3565	AGGGCTGCATGCTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCAGTGT
Db	3601	AGGGCTGCATGCTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCAGTGT
Qy	3625	AAGGCTGAGTGTTCAGACACCTGCGCTTCTCACTTCCCAACAGGCTGGGCGCT
Db	3661	AAGGCTGAGTGTTCAGACACCTGCGCTTCTCACTTCCCAACAGGCTGGGCGCT
Qy	3685	CACCCGAGGCGCAGCTTTCCCTACACAGGAGCCGGCTTCCACTCCCAACATAT
Db	3721	CACCCGAGGCGCAGCTTTCCCTACACAGGAGCCGGCTTCCACTCCCAACATAT
Qy	3745	TCCATCCCCAGATTGCGCAATGTTTCAACCCTCGCCCTGCCCTCTTGGCTTC
Db	3781	TCCATCCCCAGATTGCGCAATGTTTCAACCCTCGCCCTGCCCTCTTGGCTTC
Qy	3805	ACCATCCAGTGGAGACCTTCAGAAAGACCCCTGGAGCTCTGGGAATTTGGAG
Db	3841	ACCATCCAGTGGAGACCTTCAGAAAGACCCCTGGAGCTCTGGGAATTTGGAG
Qy	3865	AGGTGTGCCCTGTACAGAGGCGAGACCTGACCTGATGGGGGTCCCTGTGTG
Db	3901	AGGTGTGCCCTGTACAGAGGCGAGACCTTGCACCTGATGGGGGTCCCTGTGTG
Qy	3925	TTGGGGGAGGTGCTGTGGGAGTAAAAATACTGAATATATGAGTTTTTTTCA
Db	3961	TTGGGGGAGGTGCTGTGGGAGTAAAAATACTGAATATATGAGTTTTTTTCA
Qy	3985	AAAAAAAAAAAAAAAAAAAA 4006
Db	4021	AAAAAAAAAAAAAAAAAAAA 4042

RESULT 2				
AX003121				
LOCUS	AX003121	4042 bp	DNA	linear
DEFINITION	Sequence 2 from Patent WO9933998.			
ACCESSION	AX003121			
VERSION	AX003121.1	GI:9926983		PAT

[illegible]

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 CTGCGCTTCATCCCAAGCTGACAGGCTGCGGCGGATTTGGAACATGAGCTGAGCTG 1980
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 GAGGACAGAGCTTCGCGAGAGAAAGAGGCGGAGCTCTCACCTCGAGGAGTGAAGG 2040
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 GACCGCGCGCTGAGCTGTA-----CAAGGTGGATGTGACGGGCGCGTACGACACCA 2244
 GACCGCGCGCTGAGCTGTA-----CAAGGTGGATGTGACGGGCGCGTACGACACCA 2280
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PR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
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KEYWORDS Unknown.
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 Harley,C.B. and Andrews,W.H.
 Human telomerase catalytic subunit
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DEFINITION	BD011070	Human telomerase catalytic subunit			
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VERSION	JP 2001081042-A/27.				
KEYWORDS	unidentified				
SOURCE	unidentified				
ORGANISM	unclassified				
REFERENCE	1 (bases 1 to 4037)				
AUTHORS	Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori, Harley,C.B. and Andrews,W.H.				
TITLE	Human telomerase catalytic subunit				
JOURNAL	Patent: JP 2001081042-A 27 27-MAR-2001; GERON CORP, UNIVERSITY TECHNOLOGY CORP				
COMMENT	OS Unidentified				
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4587
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: March 1, 2004, 14:21:25
.5 secs

GenCore version 5.1.6
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leic search, using sw model

February 29, 2004, 19:45:38 ; Search time 8119.94 Seconds
(without alignments)
17359.183 Million cell updates/sec

US-09-424-686F-9
4006

1 gtttcaggcagctgcgtc.....aaaaaaaaaaaaaaaaaaaaa 4006

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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hits satisfying chosen parameters: 75154660

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pending Patents: NA Main.*

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Pred. No. is the number of results predicted by chance to have
score greater than or equal to the score of the result being
and is derived by analysis of the total score distribution.

SUMMARIES

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98.5	4037	20	US-09-432-503-343	Sequence 343, App
98.5	4037	31	US-09-721-477-343	Sequence 343, App
98.5	4037	31	US-09-721-506-343	Sequence 343, App
98.5	4038	13	US-10-325-810-343	Sequence 117, App
98.5	4038	13	US-08-974-524E-117	Sequence 117, App
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ALIGNMENTS

plication US/09424686F

ATION:

gen, Gustav
iegmund, Hans-Ulrich
eichel, Walter
ick, Maresa
ubov, Dmitry

NTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and Therap

NTION: Use

E: Bayer 10,203

CATION NUMBER: US/09/424, 686F

G DATE: 1999-11-29

TION NUMBER: PCT/EP98/03468

DATE: 1998-06-09

ID NOS: 32

rosoft Word

LENGTH: 4006
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(4006)
OTHER INFORMATION: Nucleotides 2184 to 2219 of SEQ ID NO. 1 have
OTHER INFORMATION: vide this sequence.
US-09-424-686F-9

Query Match 100.0%; Score 4006; DB 20; Length 4006;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4006; Conservative 0; Mismatches 0; Indels 0;

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QY	181	AGCGCGGGAGCCCGCGGCTTTCCGCGCGCTGCTGGCGCGCTGCTGCTGCTGCGG
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QY	481	TGCTGCGCGCGTGTGGGCGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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[illegible]

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Qy	2101	TGCTGGGCGTGGACGATATCCACAGGCGCTGGCGCACTTCGTGCTGCGTGC	
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Qy	2941	GCAAACTCTTTGGGGTCTTGGGCTGAAGTGTACAGCGCTGTTTCTGGATTTG	
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RESULT 3					
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; GENERAL INFORMATION:					
; APPLICANT: Hagen, Gustav					
; APPLICANT: Siegmund, Hans-Ulrich					
; APPLICANT: Weichel, Walter					
; APPLICANT: Wick, Maresa					
; APPLICANT: Zubov, Dmitry					
; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its I					
; TITLE OF INVENTION: Use					
; FILE REFERENCE: Bayer 10,203					
; CURRENT APPLICATION NUMBER: US/09/424,686F					
; CURRENT FILING DATE: 1999-11-29					
; PRIOR APPLICATION NUMBER: PCT/EP98/03468					
; PRIOR FILING DATE: 1998-06-09					
; NUMBER OF SEQ ID NOS: 32					
; SOFTWARE: Microsoft Word					
; SEQ ID NO 1					
; LENGTH: 4042					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
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Query Match 98.9%; Score 3960; DB 20; Length 4042;					
Best Local Similarity 99.1%; Pred. No. 0;					
Matches 4006; Conservative 0; Mismatches 0; Indels 36;					
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QY	61	CQATGCGCGCGCTCCCCGCTGCCAGCGCTGCGTGCTCCCTGTGTGGCAGCCACT			
Dd	61	CQATGCGCGCGCTCCCCGCTGCCAGCGCTGCGTGCTCCCTGTGTGGCAGCCACT			
QY	121	AGTGTGTGCGCTGGCCAGCTTGTGTGGCGGCTGTGGGCCCCAGGGCTGTGGCG			
Dd	121	AGTGTGTGCGCTGTGGCACGTTGTGTGGCGGCTTTCGGCGCGCTGGTGCCCAAGTGCTGTGGTGG			
QY	181	AGCGCGGGACCCGGCGGCTTTCCGCGCGCTGTGTGGTCCCAGTGCTTGTTGGTGTC			
Dd	181	AGCGCGGGACCCGGCGGCTTTCCGCGCGCTGTGTGGTCCCAGTGCTTGTTGGTGG			
QY	241	GGGACGACGGCGGCCCCCGCGGCTTCCCTTCGCGAGGTGCTTCGCTGTG			
Dd	241	GGGACGACGGCGGCCCCCGCGGCTTCCCTTCGCGAGGTGCTTCGCTGTGCTGCTGTG			
QY	301	TGGTGGCCCCAGTGTGTGCAGAGGCTGTGCGAGGCGGCGCGAAGACGTTGCTG			
Dd	301	TGTGTGGCCCCAGTGTGTGCAGAGGCTGTGCGAGCGGCGCGAAGAACGTTGCTG			
QY	361	GCTTTCGCGCTGTGGAACGGGGGCCCGGGGGGCCCCCCCCCGAGGCTTTCACACCF			
Dd	361	GCTTTCGCGCTGTGTGAACGGGGGCCCGGGGGGCCCCCCCCCGAGGCTTTCACACCF			
QY	421	GCAGCTACCTGCCAAACACGCTGACCGACGCTGCGGGGGAGCGGGGGGTGG			
Dd	421	GCAGCTACCTTGCCCAACACGGTGAACCGACGCTGCGGGGGAGCGGGGGGTGG			
QY	481	TGCTGGCGCGCTGGGCGACGACGTGCTGGTTTCACTGTGTCGACGCTGCGGCG			
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: Sequence 2, Application US/09582246
: GENERAL INFORMATION:
: APPLICANT: Bayer Aktiengesellschaft
: APPLICANT: Hegen, Gustav
: APPLICANT: Wick, Maresa
: APPLICANT: Zubov, Dmitry
: TITLE OF INVENTION: Regulation of the Gene for the
: TITLE OF INVENTION: Subunit, and Their Diagnostic and Therapeutic
: FILE REFERENCE: Lea 32 805
: CURRENT APPLICATION NUMBER: US/09/582,246
: CURRENT FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: PCT/EP98/08216
: PRIOR FILING DATE: 1998-12-22
: PRIOR APPLICATION NUMBER: DE19757984.1
: PRIOR FILING DATE: 1997-12-24
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 4042
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-582-246-2

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Query Match	98.9%	Score 3960	DB 24	Length 4042
Best Local Similarity	99.1%	Pred. No. 0		
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RESULT 5
 US-08-974-549-343
 ; Sequence 343 Application US/08974549
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin B.
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 726
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMEUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
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 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,549
 ; FILING DATE: 19-NOV-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/854,050
 ; FILING DATE: 09-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/911,312
 ; FILING DATE: 14-AUG-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/912,951
 ; FILING DATE: 14-AUG-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/915,503
 ; FILING DATE: 14-AUG-1997
 ; PRIOR APPLICATION DATA:


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CATION DATA:
ON NUMBER: WO PCT/US97/17885
TE: 01-OCT-1997
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ION NUMBER: 36,429
/DOCKET NUMBER: 015389-002610US
CATION INFORMATION:
: (415) 576-0200
(415) 576-0300
OR SEQ ID NO: 343:
ARACTERISTICS:
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56..3454
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98.5%; Score 3946.6; DB 13; Length 4037;
 identity 98.9%; Pred. No. 0;
 Conservative 4; Mismatches 3; Indels 36; Gaps 1;

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3 Application US/09432503
FORMATION:
NT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
OF INVENTION: Human Telomerase Catalytic Subunit
OF SEQUENCES: 727
ORNDENCE ADDRESS:
DRESSES: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, Eighth Floor
TY: San Francisco
ATE: California
UNTRY: USA
P: 94111-3834
R READABLE FORM:
DIUM TYPE: Floppy disk
MUTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
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LING DATE: 02-Nov-1999
ASSIFICATION: <Unknown>
APPLICATION DATA:
PLICATION NUMBER: 08/974,549
LING DATE: <Unknown>
PLICATION NUMBER: US 08/844,419
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LING DATE: 25-APR-1997
PLICATION NUMBER: US 08/851,843
LING DATE: 06-MAY-1997
PLICATION NUMBER: US 08/854,050
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PLICATION NUMBER: US 08/911,312
LING DATE: 14-AUG-1997
PLICATION NUMBER: US 08/912,951
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LING DATE: 14-AUG-1997
PLICATION NUMBER: WO PCT/US97/17618
LING DATE: 01-OCT-1997
PLICATION NUMBER: WO PCT/US97/17885
LING DATE: 01-OCT-1997
Y/AGENT INFORMATION:
ME: Apple, Randolph Ted
GISTRATION NUMBER: 36,429
FERENCE/DOCKET NUMBER: 015389-002610US
MUNICIPATION INFORMATION:
LEPHONE: (415) 576-0200
LEFAX: (415) 576-0300
FOR SEQ ID NO: 343:
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NGTH: 4037 base pairs
PE: nucleic acid
RANDEDNESS: single
POLOGY: linear

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Application US/09721477
INVENTOR:
Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru

Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,477
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FEATURE:
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APPLICATION DATA:

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AGING DATE: 22-NOV-2000

APPLICATION DATA:

AGING DATE: 01-OCT-1996

ING DATE: 18-APR-1997

ING DATE: 25-APR-1997

ING DATE: 06-MAY-1997

ING DATE: 09-MAY-1997

AGING DATE: 14-AUG-1997

AGING DATE: 14-AUG-1997

AGING DATE: 14-AUG-1997

ING DATE: 01-OCT-1997

ING DATE: 01-OCT-1997

ME: Apple, Randolph Tech

REFERENCE/DOCKET NUMBER:

TELEPHONE: (415) 576-0200

FOR SEQ ID NO: 343:

VGTH: 4037 base pairs

ANDEDNESS: single

3 TYPE: cDNA

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OTHER INFORMATION: /note

Item	Score
1. The first step in the process of creating a new product is to identify a market need.	98.5%
2. The second step in the process of creating a new product is to develop a prototype.	98.5%
3. The third step in the process of creating a new product is to conduct market research.	98.5%
4. The fourth step in the process of creating a new product is to develop a business plan.	98.5%
5. The fifth step in the process of creating a new product is to secure financing.	98.5%
6. The sixth step in the process of creating a new product is to manufacture the product.	98.5%
7. The seventh step in the process of creating a new product is to distribute the product.	98.5%
8. The eighth step in the process of creating a new product is to monitor sales and customer feedback.	98.5%
9. The ninth step in the process of creating a new product is to make improvements based on customer feedback.	98.5%
10. The tenth step in the process of creating a new product is to re-evaluate the market and adjust the product accordingly.	98.5%

Conservative 4; Mi

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```

```

3
Application US/10325810
MARION:
ATTORNEY: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
INVENTION: Human Telomerase Catalytic Subunit
OF SEQUENCES: 633
DNDENCE ADDRESS:
DRESSEE: Townsend and Townsend and Crew LLP
REF: Two Embarcadero Center, Eighth Floor
TY: San Francisco
ATE: California
NTRY: USA
P: 94111-3834
3 READABLE FORM:
DIUM TYPE: Floppy disk
MPUTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: Patent In Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/10/325,810
LING DATE: 20-Dec-2002
ASSIFICATION: <Unknown>
PLICATION DATA:
PLICATION NUMBER: US/09/402,181
LING DATE: 29-Sep-1997
PLICATION NUMBER: US/08/724,643
LING DATE: 01-Oct-1996
PLICATION NUMBER: US/08/844,419
LING DATE: 18-Apr-1997
PLICATION NUMBER: US/08/846,017
LING DATE: 25-Apr-1997
PLICATION NUMBER: US/08/851,843
LING DATE: 06-May-1997
PLICATION NUMBER: US/08/854,050

```

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FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note= "refined sequence of hTERT c
SEQUENCE DESCRIPTION: SEQ ID NO: 343:
US-10-325-810-343
Query Match 98.5%; Score 3946.6; DB 49; Length 4037
Best Local Similarity 98.9%; Pred. No. 0;
Matches 3992; Conservative 4; Mismatches 3; Indels 36;
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DB 541 GGCTCCCGAGCTGCGCTTACAGGCTGCGGGCGCGCGCGCTGCTGCTGCTGCTGCTGCT

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1-524E-117
 Case 117, Application US/08974524E
 SERIAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Telomerase Reverse Transcriptase
 NUMBER OF SEQUENCES: 477
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,524E

FILING DATE: 19-NOV-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

FILING DATE: 01-OCT-1998
APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/954 050

APPLICATION NUMBER: US 08/854,030
FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO 96/11887/1

APPLICATION NUMBER: WO PCT/US97/1
FILING DATE: 01-OCT-1997

FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/11711

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Einhorn, Gregory P.

REGISTRATION NUMBER: 38,440

REFERENCE/DOCKET NUMBER: 015389-00

TELECOMMUNICATION INFORMATION:
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TELETYPE: (415) 376-0300
INFORMATION FOR SEO ID NO: 117:

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E CHARACTERISTICS:
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 PE: nucleic acid
 RANDEDNESS: single
 POLOGY: linear
 E TYPE: cDNA
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ME/KEY: CDS
CATION: 56..3454
HER INFORMATION: /note= "refined hTERT DNA sequence"
E DESCRIPTION: SEQ ID NO: 117:
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98.5%; Score 3946.6; DB 13; Length 4038; ilarity 98.9%; Pred. NO. 0; Conservative 4; Mismatches 3; Indels 36; Gaps 1	AGCGTGTGCTCTGTGCGCACGTGGGAAGCCCTGGCGCCCGGCCACACCCCGCGATGCC 67 AGCGTGTGCTCTGTGCGCACGTGGGAAGCCCTGGCGCCCGGCCACACCCCGCGATGCC 60 GCGTCTCCCGCTGCGGAGCGGTGCGTCTCTGTGTCGCGAGCACTACCGCGAGTGTCT 127 GCGTCTCCCGCTGCGGAGCGGTGCGTCTCTGTGTCGCGAGCACTACCGCGAGTGTCT 120 CGCTTGGCCACGCTTGTGTCGGCGCTGCGGCGCCCGGAGGCTGCGGCGTGTGTCGCGAGCGGG 187 CGCTTGGCCACGCTTGTGTCGGCGCTGCGGCGCCCGGAGGCTGCGGCGTGTGTCGCGAGCGGG 180 ACCCGCGGGCTTTTCGCGCGCTGTGTGCGCCAGTGCCTGTGTGTGTCGTCGCCCTGGGAGCGC 247 ACCCGCGGGCTTTTCGCGCGCTGTGTGCGCCAGTGCCTGTGTGTGTCGTCGCCCTGGGAGCGC 240 GGCGCGCCCGCGCGCGCCCTCTCTTCGCGCAGGTGTCTGCTGAAGAGCTGTGTGCGC 307 GCGCGCCCGCGCGCGCCCTCTCTTCGCGCAGGTGTCTGCTGAAGAGCTGTGTGCGC 300 GAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGAAGACGTGCTGGCCTTCGGCTTCGCGC 367 GAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGAAGACGTGCTGGCCTTCGGCTTCGCGC 360 TGTGTGAGCGGGGCCCGCGGGGGCCCCCGCGAGGCTTTACACACAGCGTGTGCGCAGCTA 427 TGTGTGAGCGGGGCCCGCGGGGGCCCCCGCGAGGCTTTACACACAGCGTGTGCGCAGCTA 420 TGCCCAACAGGTGACCGGACGCACTGCGGGGAGCGGGGGTGTGGGGCTGTCTGCTGCG 487 TGCCCAACAGGTGACCGGACGCACTGCGGGGAGCGGGGGTGTGGGGCTGTCTGCTGCG 480 CGTGTGGCGGACGAGCTGCTGTTTCACTGTGTGGCAGCTGCGGCTCTTTGTGCTGCT 547 CGTGTGGCGGACGAGCTGCTGTTTCACTGTGTGGCAGCTGCGGCTCTTTGTGCTGCT 540 CTCCAGCTGGGCTTACAGGTGTGTGGGCGCGCGCTGTACAGCTGTGGCGCTGTGCCAC 607 CTCCAGCTGGGCTTACAGGTGTGTGGGCGCGCGCTGTACAGCTGTGGCGCTGTGCCAC 600 AGGCCGCGCCCCCGCCACACGCTAGTGGACCCCGAAGGGCTCTGGGATGCGAACGCGGC 667 AGGCCGCGCCCCCGCCACACGCTAGTGGACCCCGAAGGGCTCTGGGATGCGAACGCGGC 660 GAAACCATAGCGTACGGGAGCGGGGTCTCCCTGTGGGCTGTCCAGCGCGGGTGTGCGAG 727 GAAACCATAGCGTACGGGAGCGGGGTCTCCCTGTGGGCTGTCCAGCGCGGGTGTGCGAG 720 GCGCGGGGCGAGTGTCCAGCGGAAGTCTGCGCTTGTGCCAAGAGGCCCGAGCGTGTGCGC 787 GCGCGGGGCGAGTGTCCAGCGGAAGTCTGCGCTTGTGCCAAGAGGCCCGAGCGTGTGCGC 780 CCTGTAGCGCGGACGCGCCGCTTGTGGGCGAGGGGTCTTGGGCGCCACCGCGGCGAGGAC 847 CCTGTAGCGCGGACGCGCCGCTTGTGGGCGAGGGGTCTTGGGCGCCACCGCGGCGAGGAC 840
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 13 GTATCCGCTGTTCCAGAAAGCGGCCATATGGGCACTGCCAAGGCCCTCAAGAGCCA 2340
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 21 AGTCCTACGTCGACGTCGACAGGGATCCCGAGGGTCCATCCTCTCCACGCTGCTCTG 2580
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 23 CGCTGTCTACGGCGACATGGAGAAACAAGCTGTTTCGGGGATTTCGGCGGACCGGCT 2640
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 36 AAGCCTGTTTTCGGAATTTGAGGTGAACAGCGCTCCAGACGGTGTGCAACCAATCTA 3031

[illegible]

Application US/08974584C

INVENTION:

INVENTOR: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

OF INVENTION: Telomerase Reverse Transcriptase

OF SEQUENCES: 479

SEQUENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
REPT: Two Embarcadero Center, Eighth Floor
NY: San Francisco
STATE: California

COUNTRY: USA

P: 94111-3834

R READABLE FORM:

DIUM TYPE: Floppy disk

MPUTER: IBM PC compatible

FTWARE: PC-DOS/MS-DOS

APPLICATION DATA: PATENTIN Release #1.0, Version #1.30

PLICATION NUMBER: US/08/974,584C

LING DATE: 19-Nov-1997

ASSIGNATION: <Unknown>

PLICATION DATA:

PLICATION NUMBER: US 08/724,643

LING DATE: 01-OCT-1996

PLICATION NUMBER: US 08/844,419

LING DATE: 18-APR-1997

PLICATION NUMBER: US 08/846,017

LING DATE: 25-APR-1997

PLICATION NUMBER: US 08/851,843

LING DATE: 06-MAY-1997

PLICATION NUMBER: US 08/854,050

LING DATE: 09-MAY-1997

PLICATION NUMBER: US 08/911,312

LING DATE: 14-AUG-1997

PLICATION NUMBER: US 08/912,951

LING DATE: 14-AUG-1997

PLICATION NUMBER: US 08/915,503

LING DATE: 14-AUG-1997

PLICATION NUMBER: WO PCT/US97/17618

LING DATE: 01-OCT-1997

PLICATION NUMBER: WO PCT/US97/17885

LING DATE: 01-OCT-1997

Y/AGENT INFORMATION:

ME: Einhorn, Gregory P.

GISTRATION NUMBER: 38,440

REFERENCE/DOCKET NUMBER: 015389-002950US

MUNICIPATION INFORMATION:

LEPHONE: (415) 576-0200

LEFAX: (415) 576-0300

FOR SEQ ID NO: 117:

E CHARACTERISTICS:

NGTH: 4038 base pairs

PE: nucleic acid

RANDEDNESS: single

POLOGY: linear

E TYPE: cDNA

ME/KEY: CDS

CATION: 56.3454

HER INFORMATION: /note= "refined hTRT DNA sequence"

E DESCRIPTION: SEQ ID NO: 117:

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98.5%; Score 3946.6; DB 13; Length 4038;

ilarity 98.9%; Pred. No. 0;

Conservative 4; Mismatches 3; Indels 36; Gaps 1;

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Qy	3032	CA	AGATCCTCTGCTGCAGCGGTACAGTTTTCAGCATGTGTGCTGCAGCTCCC
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Qy	3092	TC	AGATTTTGAAGAACCCACATTTTTCTGCGCGTCACTCTCTGAACGGG
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Qy	3152	CT	CTACTCCATCCTCAAAAGCAAGAACAGCGATGTCGCTGGGGGCCAAGGG
Db	3181	CT	CTACTCCATCCTCAAAAGCAAGAACAGCGATGTCGCTGGGGGCCAAGGG
Qy	3212	CG	CGCTCTGCCCTCCGAGGCGGTGACGTGGTGTGCAACCAAGCATTTCTGCT
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UB-09-424-686f-9.rnrm

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Counter, Christopher M.
Meyerson, Matthew
Weinberg, Robert A.
VENTION: Telomerase Catalytic Subunit Gene and
NCE ADDRESS:
: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
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IA
USA
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ADABLE FORM:
PE: Floppy disk
IBM PC compatible
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; APPLICANT: Cech, Thomas R.			
; APPLICANT: Lingner, Joachim			
; APPLICANT: Nakamura, Toru			
; APPLICANT: Chapman, Karen B.			
; APPLICANT: Morin, Gregg B.			
; APPLICANT: Harley, Calvin B.			
; APPLICANT: Andrews, William			
; TITLE OF INVENTION: Telomerase Reverse Transcriptase			
; NUMBER OF SEQUENCES: 170			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend and Crew LLP			
; STREET: Two Embarcadero Center, Eighth Floor			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: USA			
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; MEDIUM TYPE: Floppy disk			
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; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/911,312			
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; ATTORNEY/AGENT INFORMATION:			
; NAME: Einhorn, Gregory P.			

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Library preparation: Dr. M. Bento Soares, University of Iowa
Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Sequencing by: Dr. M. Bento Soares, University of Iowa
Distribution: MGC clone distribution information can be
through the I.M.A.G.E. Consortium/LLNL at:
//image.llnl.gov
clone was contributed by the Brain Molecular Anatomy Project

primer: pYX-5.

Location/Qualifiers

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Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCACCAC. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

12.5%; Score 500.2; DB 13; Length 851;

ilarity 75.1%; Pred. No. 5.1e-52;

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QY 3067 CATGTGTGCT 3076
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LOCUS

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ACCESSION AW270031

VERSION AW270031.1 GI:6657061

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project

Tumor Gene Index

Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rc@mail.nih.gov

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Pranc
I.M.A.G.E. Consortium DNA Sequencing by: Washington Univ
Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution informat
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 416.

FEATURES

source

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Location/Qualifiers

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Library constructed by Life Technologies."

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 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

10.5%; Score 419; DB 12; Length 851;
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QY 3341 GAAGCTCCCGGAGGAGCGTGAAGTCCCTGGAGCGCGACCCAGCCAGCGGCACT
 Db 748 GAAGCTCGAGAGGCGGACATGACCATGCTTTACAGCTGCAGCTGACCCAGACCT

QY 3401 AGACTTCAAGACCATCTCTGGAGTGA 3425
 Db 808 AGACTTTCAGGACCATTTGGGACTAA 832

RESULT 9
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 LOCUS
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 mRNA sequence.

ACCESSION AW276315
 VERSION AW276315.1 GI:6663345
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
 1 (bases 1 to 416)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project
 Tumor Gene Index

REFERENCE
 AUTHORS Contact: Robert Strausberg, Ph.D.
 TITLE Email: cgapbs-remail.nih.gov
 JOURNAL Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael
 COMMENT Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
 Technologies, Inc. cDNA Library Arrayed by: Christa Pran
 I.M.A.G.E. Consortium DNA Sequencing by: Washington Univ
 Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution informa
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco
 High quality sequence stop: 413.

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 Site 2: NotI; Cloned unidirectionally. Primer:
 Library constructed by Life Technologies."

ORIGIN
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 Best Local Similarity 100.0%; Pred.No. 1.3e-41;
 Matches 416; Conservative 0; Mismatches 0; Indels 0;

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QY 3625 AAGGCTGAGTGTCCAGCACACCTTCCCTTCTTCACTTCCCCACAGGCTGGCGCT
 Db 356 AAGGCTGAGTGTCCAGCACACCTTCCCTTCTTCACTTCCCCACAGGCTGGCGCT

QY 3685 CACCCAGGCGGCGAGCTTTTCTACAGGAGCGCGGCTTCCATCCCAACATAG
 Db 296 CACCCAGGCGGCGAGCTTTTCTACAGGAGCGCGGCTTCCATCCCAACATAG

QY 3745 TCCATCCCGAGATTGCGCATTTGTTCACCCCTCGCCCTGCGCTTGTGCTTCC
 Db 236 TCCATCCCGAGATTGCGCATTTGTTCACCCCTCGCCCTGCGCTTGTGCTTCC

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1296
1296.1 GI:1924194

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 /lab_host="DH10B"
 /clone_lib="NCI CGAP GCBI1"
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 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD+),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (GIBCO). cDNA synthesis was
 primed with a Not I - oligo (dT) primer
 [5'-TGTTACCAATGAAGGGAGCGCGCTCATTTTTTTTTT-3',
]. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p7T3 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo. "

CAAGTTCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGTCCTTTCTTT 1745
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 CAAGTTCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGTCCTTTCTTT 60

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[illegible]

Email: C240ps-remail.hn.h.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, Universi
 cDNA Library Arrayed by: Dr. M. Bento Soares, Universi
 Cloning Sequencing by: Dr. M. Bento Soares, University of I
 Clone Distribution: Distribution information can be fou
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anato
 (BNAP)
 Seg primer: DYX-5.

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FEATURES
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/clone_11b="NIH_BMAP_FYU"
/note="Organ: Brain; Vector: pYX-Asc; Site 1:
Site 2: Not 1; The library was constructed acco
Ronald, Lennon and Soares, Genome Research, 6:
1996. Denatured RNA was size fractionated on a
gel. First strand cDNA synthesis was primed wit
primer containing a Not I site. Double strand c
size selected according to mRNA size fraction,
with EcoR I adaptor, digested with NotI and the
directionally into pYX-Asc vector. The library
sequence located between the Not I site and the
is AGCGAGACAG. This library was created for the
Iowa Brain Anatomy Project (BMAP): 'Gene Discov
Developing Mouse Nervous System', supported by I
Institute of Mental Health (NIMH), Hemin Chin.

program coordinator."

8.6%; Score 346.2; DB 14; Length 688;
 ilarity 73.9%; Pred.No. 4e-33;
 Conservative 0; Mismatches 155; Indels 0; Gaps 0;
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[069 649 bp mRNA linear EST 12-SEP-2003
 -FY0-cgp-c-19-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 3:30355746 5', mRNA sequence.
 [069
 [069.1 GI:34583033

musculus (house mouse)

Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 ilia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 bases 1 to 649)
 NCBI Institutes of Health, Mammalian Gene Collection (MGC)
 ublished (1999)
 act: Robert Strausberg, Ph.D.
 l: cgabbs-r@mail.nih.gov
 ie Procurement: Dr. Jim Lin, University of Iowa
 A Library preparation: Dr. M. Bento Soares, University of Iowa
 A Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 Sequencing by: Dr. M. Bento Soares, University of Iowa
 ie Distribution: Distribution information can be found at
 ://genome.uiowa.edu/distribution/mousefl.html
 ; clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5
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 Site 2: Not 1; The library was constructed acco
 Bonaldo, Lennon and Soares, Genome Research, 6:
 1996. Denatured RNA was size fractionated on a
 gel. First strand cDNA synthesis was primed wit
 primer containing a Not I site. Double strand c
 size selected according to mRNA size fraction,
 with EcoR I adaptor, digested with NotI and the
 directionally into pYX-Asc vector. The library
 sequence located between the Not I site and the
 is AGCAGACAG. This library was created for the
 Iowa Brain Anatomy Project (BMAP): 'Gene Discov
 Developing Mouse Nervous System', supported by
 Institute of Mental Health (NIMH), Hemin Chin,
 program coordinator."

ORIGIN

Query Match	Best Local Similarity	Score	DB	Length
47	CCCAGCACC	8.5%;	Score 340.4;	DB 14; Length 649;
26	CCCAGCACC	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
107	CAGCACC	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
86	CAGCACC	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
167	CTGCGCT	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
146	CAGCACC	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
227	GCTGCTG	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
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326	CGTCTG	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
407	CACACAC	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
386	CACCTAG	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
467	GGCGT	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
446	TGCAT	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
527	CTGCG	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;
506	CTGTG	77.3%;	Pred. No. 2.1e-32;	Mismatches 413; Conservative 0; Indels 0;

RESULT 13
 BB618671

8671 599 bp mRNA linear EST 26-OCT-2001
 8671 RIKEN full-length enriched, 8 days embryo Mus musculus
 clone 5730412M20 5', mRNA sequence.
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 8671.1 GI:16458173

musculus (house mouse)
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 bases 1 to 599)
 a.T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
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 da, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
 N Mouse ESTs (Arakawa, T., et al. 2001)
 blished (2001)
 act: Yoshinide Hayashizaki
 ratory for Genome Exploration Research Group, RIKEN Genomic
 nces Center (GSC), Yokohama Institute
 Institute of Physical and Chemical Research (RIKEN)
 22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 81-45-503-9222
 81-45-503-9216
 1: genome-resseqsc.riken.go.jp,
 http://genome.gsc.riken.go.jp/
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 M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 malization and subtraction of cap-trapper-selected cDNAs to
 are full-length cDNA libraries for rapid discovery of new
 s. Genome Res. 10 (10), 1617-1630 (2000)
 i, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 hiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
 uura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.,
 Hayashizaki, Y.
 EN integrated sequence analysis (RISA) system--384-format
 encing pipeline with 384 multicapillary sequencer. Genome Res.
 11), 1757-1771 (2000)
 no.H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
 hara, Y. and Hayashizaki, Y.
 uted-based methods for the mouse full-length cDNA
 clopedia: real-time sequence clustering for construction of a
 edundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 do.S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
 wa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 shizaki, Y.
 putational Analysis of Full-Length Mouse cDNAs Compared with
 n Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 ase visit our web site (http://genome.gsc.riken.go.jp) for
 ner details.
 use tissues.
 Location/Qualifiers
 1..599
 /organism="Mus musculus"
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 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGAGATCCAGAGCTCTTTTITTTTTTITVN 3'], cDNA was

prepared by using trehalose thermo-activated r
 transcriptase and subsequently enriched for fu
 cap-trapper. cDNA went through one round of su
 Rot = 100.0 Second strand cDNA was prepared wi
 primer adapter of sequence [5'
 GAGAGAGATTCGAGTTAATTAATTAATCCCCCCCCCC
 was cloned into the XhoI and BamHI sites. Vect
 modified pBluescript KS(+) after bulk excision
 FLC I. Cloning sites, 5' end: Sali; 3' end: Bar

ORIGIN

Query Match 8.0%; Score 322; DB 10; Length 599;
 Best Local Similarity 74.9%; Pred. No. 3.8e-30;
 Matches 403; Conservative 0; Mismatches 135; Indels 0;

QY 9 CAGCGTCTGGTCTCTGCTGGCGACAGTGGGAGCCCTGGCCCGGCCACACCCCGGAC
 Db 61 CACCCCTTGATCTTGGTTCCCGCACAGTGGGAGGCCCATCCCGGCTTGAGCAG
 QY 69 CGCGTCTCCCGCTGCGGAGCCGCTGCTCTCTGCTGGCAGGCACCTACCGCGAC
 Db 121 CGCGTCTCTCTGTTGCCCGCGGTGGCGCTCTCTGCTGGCAGGCAGTACCGGAC
 QY 129 CGCGTGGCCACGTTGCTGGCGGCGCTGGGGCCCCCAGGGCTGGCGGCTGGTGCAC
 Db 181 CGCGTGGCCACCTTTGCTGGCGGCGCTGGGGCCCCCAGGGCGGCGGCTTTGGCA
 QY 189 GACCCGCGCGCTTTCCGCGCGCTGGTGGGCCAGTGCCTGCTGTGCTGCGCTCTGC
 Db 241 GACCCGAGAGATCTACCGGCACTTTGGTTGCCCAATGCCTAGTGTGCACTGACTGG
 QY 249 CGCGCGCCCCCGCGCGCCCCCTCTCTCCGCCAGGTGCTCTGCTGAAGAGGCTG
 Db 301 CAGCCTCCACCTGCGGACCTTTCTTCCACCAAGTGTCTATCCCTGAAAGAGCTG
 QY 309 CGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGGAGAGAGCTGCTGGCTCTGGC
 Db 361 AGGGTTGTGACAGACTCTGCGAGGCGCAACAGAGAGAAACGTGCTGGCTTTGGC
 QY 369 CTGCTGGAGCGGGCGCGGGGGCGCCCCCGAGAGGCTTCCACCACAGCGTGGCG
 Db 421 CTGCTTACGAGCGCAGAGGGCGGGCTCCCATGGGCTTCACTAGTAGCGTGGCTG
 QY 429 CTGCTCCACACAGCTGACCGACGCACTGGCGGGGAGCGGGGCGTGGGGGCTGCTG
 Db 481 TTGCCCAACACCTGTTATTAGAGACCCCTGGGTGTCAGTGGTGCATGATGCTACTG
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 LOCUS
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 IMAGE:5409222, mRNA sequence.
 ACCESSION
 BQ258274
 VERSION
 BQ258274.1
 GI:20459030
 KEYWORDS
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 SOURCE
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 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
 1 (bases 1 to 664)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 cDNA Library Preparation: J. Baker (Stanford University)
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium/LLNL

Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 image.llnl.gov
 1845958
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 Location/Qualifiers
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 size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
 University)."

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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
 1 (bases 1 to 340)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David
 Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fa
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequenc
 Clone Distribution: NCI-CGAP clone distribution informa
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html
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 Location/Qualifiers
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 was prepared from human tonsillar cells enrich
 germinal center B cells by flow sorting (CD20+
 provided by Dr. Louis M. Staudt (NCI), Dr. Davi
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthe
 primed with a Not I oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGAGCGCCCTCATTTTCTTTT
]. Double-stranded cDNA was ligated to Eco RI a
 (Pharmacia), digested with Not I and cloned into
 and Eco RI sites of the modified p773 vector.
 went through one round of normalization, and wa
 constructed by Bento Soares and M. Fatima Bonal
 ORIGIN
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 Best Local Similarity 99.1%; Pred. No. 2.2e-29;
 Matches 339; Conservative 0; Mismatches 1; Indels 2;
 QY 3656 TCACCTCCCCACAGCTGGCGCTCCAGCTCCACCCAGGCGAGCTTTCTCTCAC
 Db 340 TCACCTCCCCACAGG-TGGCGCTCGGCTCCACCCAGGCGAGCTTTCTCTCAC
 QY 3716 CCGCGCTTCACCTCCCCACATAGGAATAGTCCATCCCGAGATTCGCGATTCTC
 Db 281 CCGCGCTTCACCTCCCCACATAGGAATAGTCCATCCCGAGATTCGCGATTCTC

2 09:53:32 2004

us-09-424-686f-9.rst

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March 1, 2004, 03:42:07
95 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

leic search, using sw model

February 29, 2004, 21:01:14 : Search time 58.8307 Seconds
(without alignments)
11471.157 Million cell updates/sec

US-09-424-686F-9
4006

1 gtttcaggcagctgcgc.....aaaaaaaaaaaaaaaaaaaaa 4006

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

164199 seqs, 84230614 residues

hits satisfying chosen parameters: 328398

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pending Patents NA New:*

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is the number of results predicted by chance to have a
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ived by analysis of the total score distribution.

SUMMARIES

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1.5	658	6	US-10-767-701-4204		Sequence 4204, Ap
1.4	637	6	US-10-767-701-25070		Sequence 25070, A
1.4	574	6	US-10-767-701-253		Sequence 253, App
1.4	40000	6	US-10-767-701-10913		Sequence 10913, A
1.4	666	6	US-10-767-701-4866		Sequence 4866, Ap
1.4	584	6	US-10-767-701-4186		Sequence 4186, Ap
1.3	570	6	US-10-767-701-2473		Sequence 2473, Ap
1.3	580	6	US-10-767-701-4466		Sequence 4466, Ap
1.3	1092	6	US-10-767-701-9739		Sequence 9739, Ap
1.3	522	6	US-10-767-701-30024		Sequence 30024, A
1.3	667	6	US-10-767-701-8805		Sequence 8805, Ap
1.3	697	6	US-10-767-701-4420		Sequence 4420, Ap
1.3	14800	6	US-10-767-701-195		Sequence 195, App
1.3	11409	6	US-10-767-701-603		Sequence 603, App
1.3	14321	6	US-10-767-701-191		Sequence 191, App
1.3	14641	6	US-10-767-701-193		Sequence 193, App
1.3	14760	6	US-10-767-701-192		Sequence 192, App
1.3	24841	6	US-10-767-701-10753		Sequence 10753, A
1.3	72779	6	US-10-767-701-10639		Sequence 10639, A
1.3	963	6	US-10-767-701-1482		Sequence 1482, Ap
1.3	667	6	US-10-767-701-4633		Sequence 4633, Ap
1.3	1165	6	US-10-767-701-12235		Sequence 12235, A
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1.3	558	6	US-10-767-701-23530		Sequence 23530, A
1.3	571	6	US-10-767-701-18773		Sequence 18773, A

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c 28 50.4 1.3 572 6 US-10-767-701-10516 Sequenc
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c 32 49.8 1.2 658 6 US-10-767-701-4204 Sequenc
c 33 49.6 1.2 659 6 US-10-767-701-4135 Sequenc
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c 36 49.4 1.2 459 6 US-10-767-701-1801 Sequenc
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c 41 48.4 1.2 666 6 US-10-767-701-4866 Sequenc
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c 44 48.2 1.2 1564 6 US-10-765-790-142 Sequenc
c 45 48.2 1.2 1725 1 PCT-IL03-01008-5 Sequenc

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ALIGNMENTS

RESULT 1

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; Sequence 8767, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules At
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 8767
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS56207_1
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Db 61 CCGCTCCCGCCCGCCCGCCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGC
QY 148 GCGCGCTGGGGCCCGCAGGCTGGCGGCTGTGTGCGTGGGAGCGACGGCGCCCGC
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QY 208 CGTGGTGGCCAGTGTGCTGTGTGCGTGGGAGCGACGGCGCCCGCCCGC
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; ATION:
; valic, David K.
; Zhou, Yihua
; ao, Yongwei
; NTION: Nucleic Acid Molecules and Other Molecules Associated With
; NTION: Plants and Uses Thereof For Plant Improvement
; E: 38-21(53535)B
; CATION NUMBER: US/10767,701
; G DATE: 2004-01-29
; ID NOS: 63128
; ;
; rghum bicolor
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; GTTCCCGCTGCG 596
; AGCGGCGCGGTGGGCGCTGTGCTG 485
; CCG 623

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; Application US/10767701
; ATION:
; valic, David K.
; Zhou, Yihua
; ao, Yongwei
; NTION: Nucleic Acid Molecules and Other Molecules Associated With
; NTION: Plants and Uses Thereof For Plant Improvement
; E: 38-21(53535)B
; CATION NUMBER: US/10767,701
; G DATE: 2004-01-29
; ID NOS: 63128
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; TYPE: DNA
; ORGANISM: Sorghum bicolor
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; OTHER INFORMATION: Clone ID: 9848339
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QY 239 CTGGGAGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCC
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QY 299 GCTGCTGCGCGCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGTGC
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; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules A;
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improve;
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 8805
; LENGTH: 667
; TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS56975_1
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QY 246 GCACG
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09:53:31 2004

us-09-424-686f-9.rnpn

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Application US/10767471
ATTION:
RGILL, Michele et al.
NTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
E: CL001505
CATION NUMBER: US/10/767,471
3 DATE: 2004-01-30
ID NOS: 50231
tSEQ for Windows Version 4.0

9
no sapiens
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1.3%; Score 52; DB 6; Length 11409;
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3CTGCGAGCGTGGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCTGCGCTGSC 136
TCCTGTCCCGCGCGCAGCGCTGCTGCGCGGTGCTTCCGCCAGCTGCCGCTGCTT 1824
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09:53:30 2004

us-09-424-686f-9.rnpb

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

leic search, using sw model

February 29, 2004, 19:58:33 ; Search time 873.268 Seconds
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US-09-424-686f-9

4006
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IDENTITY NUC

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Minimum Match 0%

Maximum Match 100%

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is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

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98.2	4015	9	US-09-990-080-1		Sequence 1, Appli
98.2	4015	9	US-09-843-676-224		Sequence 224, App
98.2	4015	9	US-09-953-052-1		Sequence 1, Appli
98.2	4015	14	US-10-053-758-224		Sequence 224, App
98.2	4015	14	US-10-208-243-1		Sequence 1, Appli
98.2	4015	14	US-10-054-295-224		Sequence 224, App
98.2	4015	14	US-10-054-611-224		Sequence 224, App
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98.2	4015	14	US-10-044-692-1		Sequence 1, Appli
98.2	4015	14	US-10-044-539-1		Sequence 1, Appli
98.2	4015	14	US-10-385-882-1		Sequence 1, Appli
94.5	4029	9	US-09-843-676-173		Sequence 173, App
94.5	4029	10	US-09-438-486-173		Sequence 173, App
94.5	4029	14	US-10-053-758-173		Sequence 173, App

16	3786.2	94.5	4029	14	US-10-054-295-173	Sequenc
17	3786.2	94.5	4029	14	US-10-054-611-173	Sequenc
18	3579	89.3	3855	14	US-10-044-692-4	Sequenc
19	3579	89.3	3855	14	US-10-044-539-4	Sequenc
20	3318	82.8	3453	14	US-10-205-629-1	Sequenc
21	3318	82.8	3453	14	US-10-105-616-1	Sequenc
22	3314	82.7	3396	9	US-09-749-728B-32	Sequenc
23	3306	82.5	8742	14	US-10-105-616-6	Sequenc
24	1898.4	47.4	2176	14	US-10-044-692-3	Sequenc
25	1898.4	47.4	2176	14	US-10-044-539-3	Sequenc
26	1815.2	45.3	2171	9	US-09-843-676-100	Sequenc
27	1815.2	45.3	2171	9	US-09-766-253-100	Sequenc
28	1815.2	45.3	2171	10	US-09-438-486-100	Sequenc
29	1815.2	45.3	2171	14	US-10-053-758-100	Sequenc
30	1815.2	45.3	2171	14	US-10-054-295-100	Sequenc
31	1815.2	45.3	2171	14	US-10-054-611-100	Sequenc
32	1741	43.5	1866	14	US-10-294-778-11	Sequenc
33	1522.8	38.0	4200	14	US-10-044-692-6	Sequenc
34	1522.8	38.0	4200	14	US-10-044-539-6	Sequenc
35	1522.8	38.0	15418	9	US-09-783-203-1	Sequenc
36	1522.8	38.0	15418	9	US-09-994-427A-1	Sequenc
37	1522.8	38.0	15418	10	US-09-995-419A-1	Sequenc
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39	1522.8	38.0	15418	14	US-10-023-969-1	Sequenc
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ALIGNMENTS

RESULT 1
US-09-733-294A-3
; Sequence 3, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TEXT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733, 294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-733-294A-3

Query Match 98.2%; Score 3933; DB 9; Length 4015;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 3979; Conservative 0; Mismatches 0; Indels 36;
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Db	1141	GACCATCTTTCTGGTTTCCAGGCCCTGGATGCCAGGGACTCCCAGCAGGTTCG	
Qy	1208	GCCCCAGCGTACTGGCAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAAACCF	
Db	1201	GCCCCAGCGTACTGGCAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAAACCF	
Qy	1268	GTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCCAGCTGCCGTCA	
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Qy	1328	AGCCGGTGTCTGTGCCCGGAGAAAGCCCAAGGCTCTGTGGCGGCCCCCGAGGA	
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Qy	1388	CACAGACCCCGGTGCGCTGTGTCAGCTGCTCCGCGAGCACAGCAGCCCTGGCA	
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Qy	1448	CGGCTTCTGTGCGGGCTGCTGCGCCGGCTGGTGCCCCAGAGCTCTCGGGGCTC	
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Qy	1508	CAACGAACCCGCTTCTCTCAGGAACCAAGAAGTTTCATCTCCCTGGGGAAAGCA	
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Qy	1748	TGTCA CGGAGACCACTTTCAAAGAACAGGCTCTTTTCTACCGGAGAGTGT	
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Qy	1808	CAAGTTGCAAGCATTTGGAATCAGACAGCACCTTGAAGAGGCTGACGTGCGGGA	
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Qy	1868	GGAAGCAGAGGTTCAGCAGCATCGGGAAGCCAGGCGCCGCTGCTGACGTCGAG	
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Qy	2192	GGACAGGCTCAGGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACACGTACTG	

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Db 3961 GAGGTGCTGTGGAGTAAATTAATGATATATAGTGTTCAGTTTGAATAA

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RESULT 3

US-09-843-676-224

; Sequence 224, Application US/09843676

; Patent No. US20020164786A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. US20020164786A1el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESS: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

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plication US/09953052
 0020173476A1

RMATION:

NT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.

F INVENTION: Antisense Compositions for Detecting and
 OF SEQUENCES: 72

ONDENCE ADDRESS:

DRESSEE: Townsend and Townsend and Crew LLP
 REET: Two Embarcadero Center, Eighth Floor
 TY: San Francisco
 ARE: California
 UNTRY: USA

P: 94111-3834

R READABLE FORM:

DIUM TYPE: Floppy disk

MPUTER: IBM PC compatible

ERATING SYSTEM: PC-DOS/MS-DOS

FTWARE: Patent In Release #1.0, Version #1.30

APPLICATION DATA:

PLICATION NUMBER: US/09/953,052

LING DATE: 14-Sep-2001

ASSIFICATION: <Unknown>

PLICATION DATA:

PLICATION NUMBER: 09/052,919

LING DATE: <Unknown>

PLICATION NUMBER: US 08/844,419

LING DATE: 18-APR-1997

PLICATION NUMBER: US 08/846,017

LING DATE: 25-APR-1997

PLICATION NUMBER: US 08/851,843

LING DATE: 06-MAY-1997

PLICATION NUMBER: US 08/854,050

LING DATE: 09-MAY-1997

PLICATION NUMBER: US 08/911,312

LING DATE: 14-AUG-1997

PLICATION NUMBER: US 08/912,951

LING DATE: 14-AUG-1997

PLICATION NUMBER: US 08/915,503

LING DATE: 14-AUG-1997

PLICATION NUMBER: US 08/974,549

LING DATE: 19-NOV-1997

PLICATION NUMBER: US 08/974,584

LING DATE: 19-NOV-1997

PLICATION NUMBER: WO PCT/US97/17618

LING DATE: 01-OCT-1997

PLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Parent, Annette S.
 REGISTRATION NUMBER: 42,058
 REFERENCE/DOCKET NUMBER: 015389-0036000US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4015 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 56...3454
 OTHER INFORMATION: /product= "human telomerase revers
 transcriptase (hTRT)"
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-953-052-1

Query Match 98.2%; Score 3933; DB 9; Length 4015;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 3979; Conservative 0; Mismatches 0; Indels 36;

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Db	61	GGCGCTCCCCGCTCCCGAGCGGCTGCTCCCTGCTGCGCAGCCACTACCGCGA
QY	128	GCGCTGGCCAGCTTCTGCGCGGCTGGGGCCCCCAGGGCTGGGGCTGGTGCA
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QY	188	GGACCCGGCGGCTTTCGCGCGCTGCTGGCCCGCAGTCTGGTGTGCTGCCCTG
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Db	241	ACGGCGCGCCCGCGCCCTCTCTCCCGCAGGTGCTCTGCTGCTGCTGCTGCTG
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Db	601	TCAGGCCCGGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGCTTGGGATCGGA
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RESULT 5

US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product="hTERT"
; /note="human telomerase reverse
; transcriptase (hTERT) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224

Query Match 98.2%; Score 3933; DB 14; Length 4015;
Best Local Similarity 99.1%; Pred. NO. 0;
Matches 3979; Conservative 0; Mismatches 0; Indels 36;

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Qy 2108 CTTGACGATATCCACAGGCGCTGCGCGCACCTTCTGCTGCTGCTGCTGCGGCGCA
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QY	3332	GCTGAGTCGGAAGCTCCCGGGACACGCTGACT	CGCCCTGGAGGGCCGACAGCCAC
Db	3361	GCTGAGTCGGAAGCTCCCGGGACGACGCTGACT	CGCCCTGGAGGGCCGACAGCCAC
QY	3392	ACTGCCCTCAGACTTCAGAGACCATCTGTGA	CTGTGATGGGCCA
Db	3421	ACTGCCCTCAGACTTCAGAGACCATCTGTGACT	GTGGCCACCCGCCCA
QY	3452	GAGCAGACACGAGCCCTGTCA	CGCCGGGCTCTACGTCCAGAGAGGGAGGG
Db	3481	GAGCAGACACGAGAGCCCTGTCA	CGCCGGGCTCTACGTCCAGAGAGGGAGGG
QY	3512	CACACCCAGCCCGCACCGCTGGGAGTCTGAG	CGCTGAGTGTGTTGGCCGA
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QY	3572	CATGTCGGGCTCAAGGCTCAGTGTCCGGCT	GAGGCTGAGCGCTGAGCGAGTGTCCAGCCA
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QY	3632	GAGTGTCCAGCACACGTGCGGCTCTTCACT	TCCCCACAGGCTGGCGCTCGGCTCC
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QY	3692	GGGCGAGCTTTTCTTCCACGAGAGCCGGCT	CTCAGCTCCCACTAGGAATAGT
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US-10-208-243-1
; Sequence 1, Application US/10208243

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1  Publication No. US20030044394A1
2  GENERAL INFORMATION:
3  APPLICANT: Gaeta, Federico C.A.
4  APPLICANT: Geron Corporation
5  TITLE OF INVENTION: Methods and Compositions for Eliciting an Imm
6  nune Response to a Telomerase Antigen
7  FILE REFERENCE: 015389-003500PC
8  CURRENT APPLICATION NUMBER: US/10/208.243
9  CURRENT FILING DATE: 2002-07-30
10 PRIOR APPLICATION NUMBER: US/09/675,321
11 PRIOR FILING DATE: 2000-09-28
12 PRIOR APPLICATION NUMBER: US 60/112,006
13 PRIOR FILING DATE: 1998-03-31
14 PRIOR APPLICATION NUMBER: WO PCT/US99/06898
15 PRIOR FILING DATE: 1999-03-30
16 NUMBER OF SEQ ID NOS: 2
17 SOFTWARE: PatentIn Ver. 2.0
18 SEQ ID NO 1
19 LENGTH: 4015
20 TYPE: DNA

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no sapiens

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6) ..(3454)

ATION: human telomerase reverse transcriptase (hTERT)

98.2%; Score 3933; DB 14; Length 4015;

ilarity 99.1%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 36; Gaps 1;

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Qy	1148	GACCATCTTCTCGGGTTCAGAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCC
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Qy	1208	GCCCCAGCGCTACTGGCAAAATGGGGCCCCCTGTTTCTGAGCTGCTTTGGGAACCF
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Qy	1328	AGCCGCTGTCTGTGCCGGGAGAGGCCACAGGGCTCTGTGGCGGCCCGCGAGGA
Db	1321	AGCCGCTGTCTGTGCCGGGAGAGGCCACAGGGCTCTGTGGCGGCCCGCGAGGA
Qy	1388	CACAGACCCCCGTGCGCTGTGTGAGCTGCTCCGCCAGCAACAGCAGCCCTGGCA
Db	1381	CACAGACCCCCGTGCGCTGTGTGAGCTGCTCCGCCAGCAACAGCAGCCCTGGCA
Qy	1448	CGGCTTCGTGGGGCCCTGCTCGCGCGGTGTGTGTGTCGCCCGAGGCTCTGGGGCTC
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Db	1681	CAAGTTCTCTGCACTGGCTGATGAGTGTGTACGTCTGAGGCTGCTCAGGTCCTTT
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Qy	1868	GGAAGCAGAGGTCAGGACATCGGGAGCCAGGCCCCCTGCTGAGCTCCAGI
Db	1861	GGAAGCAGAGGTCAGGACATCGGGAGCCAGGCCCCCTGCTGAGCTCCAGI
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Db	1921	CTTCATCCCCAACGCTGACGGGCTCGCGGCCATTTGTGAAATGACATGACGTCTGK
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DB	2461	CAGTGGGCTCTTTTCGACGCTCTCTCTACGCTTTCATGTGCGCACCAAGCGCGTGGGCA
QY	2492	CAAGTCTCATAGTCCAGTCCAGGCGGATCCCGCAGGGCTCCATCTCTCCAGGC
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QY	2552	CAGCTCTGTCTACCGCGACATGGAGAACAAAGCTGTTTGGCGGGATTTCCGGCGGG
DB	2581	CAGCTCTGTCTACCGCGACATGGAGAACAAAGCTGTTTGGCGGGATTTCCGGCGGG
QY	2612	GCTCTCTGGTTTGGTGTGATGATTTCTTTGGTGTGACACTCACCTCACCCACG
DB	2641	GCTCTCTGGTTTGGTGTGATGATTTCTTTGGTGTGACACTCACCTCACCCACG
QY	2672	CTTCTCTCAGGACCTCGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTT
DB	2701	CTTCTCTCAGGACCTCGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTT
QY	2732	GACAGTGGTGAACCTTCCCTCTAGAAGACGAGGCCCTGGGTGGCACGCGTTTTCG
DB	2761	GACAGTGGTGAACCTTCCCTCTAGAAGACGAGGCCCTGGGTGGCACGCGTTTTCG
QY	2792	GCCGGCCCAAGGCTATTTCCCTTGGTGGCGCTGTGCTGGATACCCGGAACCT
DB	2821	GCCGGCCCAAGGCTATTTCCCTTGGTGGCGCTGTGCTGGATACCCGGAACCT
QY	2852	GCAGAGGATCTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTT
DB	2881	GCAGAGGATCTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTT
QY	2912	CGGCTTCAAGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGTGGCACGCGTTTGT
DB	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGTGGCACGCGCT
QY	2972	TCAAGGCTCTTTCTGATTTGCAAGTGAAAGCCTCCAGACGGTGTGACCAAF
DB	3001	TCAAGGCTCTTTCTGATTTGCAAGTGAAAGCCTCCAGACGGTGTGACCAAF
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DB	3061	CAAGATCTCTCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGCTGACGTCTCC
QY	3092	TCAGCAAGTTTGAAGAACCCCACTTTTTTCTGCGCGTCACTCTGTGACACGGC
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QY	3212	CGGCGCTCTGCCCTCGAGGCGGTGCGAGTGTGCGCACCAAGACAATCTCTGCT
DB	3241	CGGCGCTCTGCCCTCGAGGCGGTGCGAGTGTGCGCACCAAGACAATCTCTGCT
QY	3272	GACTCGACACCGGTGTCACCTACGTGCGACTCTCTGGGTCACTCAAGACAGCCCA
DB	3301	GACTCGACACCGGTGTCACCTACGTGCGACTCTCTGGGTCACTCAAGACAGCCCA
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DB	3361	GCTGAGTCGAAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGCCGAGGCCAA
QY	3392	ACTGGCCTCAGACTTCAAGACCATCTCTGGAATGATGGCCAACCGGCCACAGCCA
DB	3421	ACTGGCCTCAGACTTCAAGACCATCTCTGGAATGATGGGCCACCGGCCACAGCCA
QY	3452	GAGCAGACACAGAGCCCTGTCAAGCGCGGCTCTACGTCCCGAGGAGGAGGG
DB	3481	GAGCAGACACAGAGCCCTGTCAAGCGCGGCTCTACGTCCCGAGGAGGAGGG
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 GGTCCTGTGGGAGTAAATACCTGAATATATAGTTTTTCAGTTTTGAAAAAAA 4015

4 Application US/10054611
US20030059787A1

Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin

ANDREWS, WILLIAM H.
F INVENTION: No. US20030059787A1el Telomerase
OF SEQUENCES: 225

NDENCE ADDRESS:
DRESSEE: Townsend and Townsend and Crew LLP
REET: Two Embarcadero Center, 8th Floor
Y: San Francisco

SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:

1GGGCGGGGGCAGTGCACGCGGAAGTCTGCGGTGGCCCAAGAGGCCCAAGGCGTGGCGC 787
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DB	1801	CAAGTTGCCAAGCAATTGGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGG	
QY	1868	GGAAGCAGAGGTCAAGCGAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGCTCCAA	
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QY	2108	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGGCCCF	
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QY	2168	GCCGCTCTGAGCTGTA-----CAI	
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QY	2612	GCTCTGCGTTTGGTGGATGATTTCTTGTGTGGTGACACTCACCTCAACCAACGC	
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RESULT 10
US-10-044-692-1
; Sequence 1, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: D1
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; Zip: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

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 Note= "human telomerase reverse
 transcriptase (hTERT) catalytic protein
 component"
 E DESCRIPTION: SEQ ID NO: 1:

98.2%; Score 3933; DB 14; Length 4015;
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Db	961	GCACCACGCGGGCCCCCATCCACATCGCGGCACACAGTCCCTTGGGACACGC
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Qy	1268	GTGCCCCCTACGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTTCCGCTCAC
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Db	1321	AGCCGCTGTCTGTGCCCGGAGAGCCCCCAGAGGCTCTGTGGCGGCCCGCAGGAG
Qy	1388	CACAGACCCCGCTCGCTGTGTGAGCTGCTCCGCCACGACACAGCAGCCCCCTGGCA
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Qy	1448	CGGCTTGTGCGGGCTGTCTGCGCGGCTGTGTGCCCGGCTGTGTGCCCGGCTCTCGGGCTCTC
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Qy	1508	CAACGAAACCGGCTTCTCTCAGGAACCAAGAAGTTCTCTCCCTGGGGGAAGCA
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Qy	1568	GCTCTCGCTGCAGAGCTGACGTGGAAGATGACGCTGCGGACATGCGCTTGGCT
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Qy	1628	GAGCCACAGGGTTGGCTGTGTTCGGCGCGGAGACACCGTCTGGGTGAGGAGAT
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Andrews, William H.
OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
OF SEQUENCES: 335
ONDENSE ADDRESS:
DRESSEE: Townsend and Townsend and Crew LLP
REF: Two Embarcadero Center, 8th Floor
TY: San Francisco
ATE: California
UNTRY: United States of America
P: 9411
R READABLE FORM:
DIUM TYPE: Floppy disk
MPUTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: Patent in Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/10/044,539
LING DATE: 11-Jan-2002
ASSIFICATION: 435
APPLICATION DATA:
PLICATION NUMBER: 08/912,951
LING DATE: <Unknown>
PLICATION NUMBER: US 08/854,050
LING DATE: 09-MAY-1997
PLICATION NUMBER: US 08/851,843
LING DATE: 06-MAY-1997
PLICATION NUMBER: US 08/846,017
LING DATE: 25-APR-1997
PLICATION NUMBER: US 08/844,419
LING DATE: 18-APR-1997
PLICATION NUMBER: US 08/724,643
LING DATE: 01-OCT-1996
Y/AGENT INFORMATION:
ME: Apple, Randolph T.
GISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
MUNICATION INFORMATION:
LEPHONE: (415) 576-0200
LEFAX: (415) 576-0300
FOR SEQ ID NO: 1:
E CHARACTERISTICS:
NGTH: 4015 base pairs
PE: nucleic acid
RANDEDNESS: single
POLOGY: linear
E TYPE: CDNA
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98.2%; Score 3933; DB 14; Length 4015;
ilarity 99.1%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 36; Gaps 1;

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Db 2521 CAAGTCTTACGTCTAGTGGCAGGGATCCCGAGGGCTCCATCTCTTCCAGCT
QY 2552 CAGCTGTGCTTACGCGCATGAGAACAAAGCTGTTTGGGGGATTCGGCGGGA
Db 2581 CAGCTGTGCTTACGCGCATGAGAACAAAGCTGTTTGGGGGATTCGGCGGGA
QY 2612 GCTCTGCGTGTGGTGGATGATTTCTTGTGGTGAACCTCACCTCACCCACGC
Db 2641 GCTCTGCGTGTGGTGGATGATTTCTTGTGGTGAACCTCACCTCACCCACGC
QY 2672 CTTCTCAGGACCTGTGTCCAGGTGTCCCTGAGTATGGCTGCGGTGGAATT
Db 2701 CTTCTCAGGACCTGTGTCCAGGTGTCCCTGAGTATGGCTGCGGTGGAATT
QY 2732 GACAGTGTGAACTTCCCTGTAGAGAGAGGCGCTGCGGTGGCAGCGCTTTGT
Db 2761 GACAGTGTGAACTTCCCTGTAGAGAGAGGCGCTGCGGTGGCAGCGCTTTGT
QY 2792 GCCGGCCACGGCTTATTTCCCTGTGGTGGCTGCTGTGTGATACCCGGACCTT
Db 2821 GCCGGCCACGGCTTATTTCCCTGTGGTGGCTGCTGTGTGATACCCGGACCTT
QY 2852 GCAGAGCAGTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTT
Db 2881 GCAGAGCAGTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTT
QY 2912 CGGCTTCAAGGCTCGGAGAACATCGCTGCGAACTCTTTGGGCTCTGGGCTT
Db 2941 CGGCTTCAAGGCTCGGAGAACATCGCTGCGAACTCTTTGGGCTCTGGGCTT
QY 2972 TCAGAGCTGTCTTCTGATTTGCAAGTGAACAGAGCTCCAGAGCGTGTGACCAA
Db 3001 TCAGAGCTGTCTTCTGATTTGCAAGTGAACAGAGCTCCAGAGCGTGTGACCAA
QY 3032 CAAGATCTCTGCTGAGGCGTACAGTTCAGGATGTGTGCTGAGCTTCC
Db 3061 CAAGATCTCTGCTGAGGCGTACAGTTCAGGATGTGTGCTGAGCTTCC
QY 3092 TCAGAGTGTGGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGCGC
Db 3121 TCAGAGTGTGGAAGAACCCACATTTTCTGCGGCTCATCTCTGACAGCGC
QY 3152 CTGCTACTCCATCTGAAAGCAAGAACAGAGGATGTGCTGCGGCGGCGGAGGCG
Db 3181 CTGCTACTCCATCTGAAAGCAAGAACAGAGGATGTGCTGCGGCGGCGGAGGCG
QY 3212 CGGCGCTCTGCCCTCGAGGCGCTGAGTGGCTGTGCGCAACAAGCATTTCTGCTC
Db 3241 CGGCGCTCTGCCCTCGAGGCGCTGAGTGGCTGTGCGCAACAAGCATTTCTGCTC
QY 3272 GACTCGACACCGTGTCACTACGTGCACTCTCTGGGCTCATCTGAGCAGACCCAG
Db 3301 GACTCGACACCGTGTCACTACGTGCACTCTCTGGGCTCATCTGAGCAGACCCAG
QY 3332 GCTGAGTTCGGAAGCTCCCGGGAGACGCTGACTGCTGGAGCGCGGAGCGCAAC
Db 3361 GCTGAGTTCGGAAGCTCCCGGGAGACGCTGACTGCTGGAGCGCGGAGCGCAAC
QY 3392 ACTGCCCTCAGACTTCAAGACCATCTCTGAGTATGGCCACCCGCGCCAGCGGAG
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTCTGAGTATGGCCACCCGCGCCAGCGGAG

CCCGCTGCCGAGCCGCTGCCGCTCCCTGCTGCCGAGCCACTACCGCGAGGTGCTGCCGC 132

Qy	788	TGCCCCTGACCGCGAGCGAGACGCCCGTTGGGCAGGGGTCTCTGGGGCCACACCGGG
Db	778	TGCCCCTGACCGCGAGCGGAGACGCCCGTTGGGCAGGGGTCTCTGGGGCCACACCGGG
Qy	848	GGGTGACCGAGTGACCGGTGGTTTCTGTGTGTGTGTCTCACTGTGCCAGACCGCGCGP
Db	838	GGCTGACCGAGTGACCGGTGGTTTCTGTGTGTGTGTCTCACTGTGCCAGACCGCGCGP
Qy	908	CACCTCTTTTGGAGGGTGCCTCTCTTGGGACGCGCCACTCCCAACCCATCCGTGGG
Db	898	CACCTCTTTTGGAGGGTGCCTCTCTTGGGACGCGCCACTCCCAACCCATCCGTGGG
Qy	968	GCACACGCGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACGCCC
Db	958	GCACACGCGGGCCCCCATCCACATCGCGGCCACCAAGT - CTTGGGACACGCCC
Qy	1028	CCGGGTGTAGCGGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAGGAGCA
Db	1017	CCGGGTGTAGCGGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAGNA -- C
Qy	1088	GGCCTCCTTCTACTTC - AGCTCTCTTGAGGCCAGAGCTGACTGGCGCTCGGAGGC
Db	1075	NGCCTCCTTCTACTCAATATATCTGAGGCCAGAGCTGACTGGCGTTCGGGAGG
Qy	1147	AGACCATCTTTCTGGGTTCAGAGCCCTTGGATGCCAGGACTCCCGCGAGTTTGC
Db	1135	GAGACANTCTTTCTGGTTCAGAGCCCTTGGATGCCA - GGATTTCCCGCAGGTTGC
Qy	1207	TGCCCCAGCGCTACTTGGGAAATGCGGCCCTCTGTTCTGTAGCTGCTTGGGAACC
Db	1194	TGCCCCAGCGENTACTTGGCAAAATGCGGCCCTCTGTTCTGTAGAGCTGCTTGGGAACC
Qy	1267	AGTGCCCTTACGGGGTGCTCTCAAGACGACTGCCCGCTGCGAGCTGCGGTCF
Db	1254	AGTGCCCTTACGGGGTGTTCTCAAGACGACTGCCCGCTGCGAGCTGCGGTCF
Qy	1327	CAGCGGTGCTGTGCCCCGGGAGAGCCCCAGGGCTCTGTGCGGCCCCCCCGAGG
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Qy	1387	-ACACAGACCCCGTGCCTGTGTGAGTGCTTCGCGCAGCA CAGCAGCCCTTGC
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Qy	1446	TACGGCTTGTGCGGSCCTGCTGCGCGGCTGTGGCCCAAGGCTCTGTGGGC
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Qy	1506	CACACGAACCGCGCTTCTCTAGGAAACACCAAGAAGTTTCATCTCCCTGGGGAAG
Db	1494	CACACGAACCGCGCTTCTCTAGGAAACACCAAGAAGTTTCATCTCCCTGGGGAAG
Qy	1566	AGCTCTCGCTGAGAGCTGAGTGGAAGATGAGCGGTGCGGGA CTGCGCTTGC
Db	1554	AAGCTCTCGCTGAGAGCTGAGTGGAAGATGAGCGGTGCGGGA CTGCGCTTGC
Qy	1626	AGGAGCCACGGGTTGGCTGTGTCGCGCGCAGACGACCGTCTGCGTGAAGG
Db	1614	AGGAGCCACGGGTTGGCTGTGTCGCGCGCAGACGACCGTCTGCGTGAAGG
Qy	1686	GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGTCT
Db	1674	GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGTCT
Qy	1746	TATGTACGGAGCACCGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAT
Db	1734	TATGTACGGAGCACCGTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAT
Qy	1806	AGCAAGTTGCAAGCATTTGGATCAGACAGCATTTGAGAGGGTGCACTGGG
Db	1794	AGCAAGTTGCAAGCATTTGGATCAGACAGCATTTGAGAGGGTGCACTGGG
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2934 CGCGGCTTCAAGGCTGGAGGAAACATGCGTCGAAACTCTTTGGGCTCTTGCGC
 2970 TGTCAACGCTGTTTCTGGATTTGAGGTGACAGCTCCAGACGGTGTGCAAC
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 3150 CTCCTCTATCTCCATCTGAAAGCAAGCAAGCAAGGATGTGCTGCGGCGCAAG
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 3894 TGCCCTGTACACAGCGAGGAGCCCTGACCTGGATGGGGTCCCTGTGGGTCAA
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 3954 GGGAGGCTGCTGGAGGTAAATACTGAATATATGAGTTTTCAGTTTGTGAAAA
 3990 AAAAAAATAAAAAA 4005
 4014 AAAAAAATAAAAAA 4029

94.5%; Score 3786.2; DB 14; Length 4029;
 ilarity 97.6%; Pred. No. 0;
 Conservative 0; Mismatches 53; Indels 45; Gaps 9;
 AGCGTCGTCCTGCTGCGCACCTGGGAAGCCCTGCGCCCGCGCACCCCGCGATGCC 67
 AGCGTCGTCCTGCTGCGCACCTGGGAAGCCCTGCGCCCGCGCACCCCGCGATGCC 60

[illegible]

GACTCGACACCGTGTCACTTACGTGGCCACTCTGTGGGTCACTCAGACAGCCAGACG 3353
 GCTGAGTCGGAAGCTCCCGGGACACGCTGACTGCCTCTGGAGGCGCAGCCAAACCG 3389
 GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCTTGGAGGCGCAGCAACCG 3413
 ACTGCCCTCAGACTTCAAGACCATCTGTGACTGATGGCCACCGCCACAGCCAGGCC 3449
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 GAGCAGACACCAAGAGCCCTGTTCACGCGGGGCTTACGTCTCCAGGAGAGGAGGGCGG 3533
 CACACCCAGGCGCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTTTGGCCGAGGCC 3569
 CACACCCAGGCGCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTTTGGCCGAGGCC 3593
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 GAGTGTCCAGCACACCTTCGCGTCTTCACTTCCCGCAGGCTGGCGCTCGGCTCACCC 3689
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 GAGGTGCTGTGGGAGTAAAACTCAATATATGAGTTTTTTCAGTTTTTGAIAAAAAAAA 4013
 AAAAAAAAAAAAAA 4005
 AAAAAAAAAAAAAA 4029

: March 1, 2004, 23:53:01
68 secs

id 36. a a but not as in
Kellie.

Query	Match	Length	DB	ID	Description
98.9	4042	2	AAV72117	Human cat	
98.5	4037	2	AAV22428	Human tel	
98.3	4023	2	AAV60320	Human tel	
98.2	4070	6	ABL53711	Human tel	
98.2	4015	2	AZ200724	Human tel	
98.2	4015	2	AZ202079	Human tel	
98.2	4015	2	AZ230154	cDNA enco	
98.2	4015	4	AAH45901	Human hTE	
98.2	4015	6	RAA46821	Human tel	
98.2	4015	6	ABA97534	Cancer ce	
98.2	4015	7	ACC58039	Human tel	
98.2	4015	7	ACC57552	Human tel	
98.2	4015	7	ABZ232474	Human tel	
98.2	4015	7	ACC44482	Human tel	
98.1	4015	2	AAZ08150	Human tel	
98.1	4015	7	ABZ18391	Group III	
98.1	4027	2	AAZ89424	Human EST	
98.1	4027	3	AAA29388	hEST2, a	
98.1	4027	9	ADC47060	Human TER	
98.1	4027	9	ADE40481	Human tel	
97.6	3918	2	AAZ18269	Telomeras	
97.6	3918	2	AAZ18278	Telomeras	
96.8	3964	2	AAZ18254	Human tel	

CC This sequence encodes a novel human catalytic telomerase sub-unit

CC This sequence encodes a novel human catalytic telomerase sub-unit.

The sequence encodes human telomerase reverse transcriptase which is a ribonucleoprotein. The present invention also includes the following methods: (A) determining whether a test compound is an inhibitor of hTERT by detecting the change in hTERT recombinant polynucleotide, on administration of the compound; (B) detection of recombinant telomerase by contacting a protein preparation of a sample with a probe complementary to the RNA component of the hTERT RNA or a telomerase RNA component; (C) detection of the hTERT RNA or a telomerase RNA component in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the complex; and correlating the presence of complex or amplification with the presence of hTERT in the sample; and (D) increasing the activity of a vertebrate cell by increasing hTERT expression; and (E) identifying an agent that causes an increase in cell vertebrate cell proliferation by testing various agents on cells and selecting an agent to create a medicament that inhibits ageing. A protein preparation of hTERT and the polynucleotide encoding hTERT can be used in the treatment of medicaments for inhibiting the effect of ageing or inhibitors of telomerase activity can be used to treat conditions associated with high telomerase activity. A protein preparation also can be used in the new methods.

Standard; cDNA; 4023 BP.

merase gene referred to as hEST2.

subunit; human; telomerase; telomere maintenance; diagnosis; cancer; ss.

OS	Homo sapiens.
XX	
FF	Location/Qualifiers
XX	59..3458
FT	/tag= a
FT	
XX	
XX	WO9837181-A2.
PX	
PD	27-AUG-1998.
XX	
PF	20-FEB-1998; 98WO-US003404.
XX	
PR	20-FEB-1997; 97US-0038750P.
PR	20-MAY-1997; 97US-0047151P.
PR	01-AUG-1997; 97US-0054549P.
PR	14-AUG-1997; 97US-0055762P.
PR	30-OCT-1997; 97US-0064322P.
XX	
PA	(WHED) WHITEHEAD INST BIOMEDICAL RES.
XX	
PI	Counter CM, Meyerson M, Weinberg RA;
XX	
DR	WPI; 1998-495367/42.
XX	P-PSDB; AAW71376.
XX	
PT	New isolated human telomerase catalytic sub-unit gene - used to
PT	products for increasing or reducing the life span of cells such
PT	cells or transformed cells.
XX	
PS	Claim 5; Fig 5A-B; 96pp; English.
XX	
CC	The present sequence encodes the catalytic subunit of a human t
CC	holoenzyme. Disruption of the telomerase gene alters telomere
CC	maintenance. The DNA is essential for telomerase activity, and
CC	protein is physically associated with telomerase and a consti
CC	tive telomerase complex. The products can be used for increas
CC	reducing the lifespan of cells such as cancer cells or transfo
CC	They can also be used in the diagnosis and treatment of malign
CC	addition, cells with a longer lifespan can be transplanted int
CC	grafted onto an individual (e.g. as skin grafts, as systems fo
CC	of therapeutic proteins, such as hormones and enzymes), to whor
CC	provide therapeutic benefit
XX	
SQ	Sequence 4023 BP; 668 A; 1363 C; 1277 G; 715 T; 0 U; 0 Other;
Query Match 98.3%; Score 3937.8; DB 2; Length 4023;	
Best Local Similarity 99.1%; Pred. No. 0;	
Matches 3985; Conservative 0; Mismatches 2; Indels 36;	
QY	5 CAGCGACGCGTGGTCCTGTCTGCACGCTGGGAGCCCTGGCCCCGGCCACCC
Dd	
Db	1 CAGCGACGCGTGCTCTGTCTGCCACGTGGGAGCCCTGGCCCCGGCCACCC
QY	65 GCCGCGCGCTCCCCTGTCCGACGCGCTGCTCCTCTGTGCGCAGCCATACC
Dd	
Db	61 GCCGCGCGCTCCCCTGTCCGACGCGCTGCTCCTCTGTGCGCAGCCATACC
QY	125 GCTGCGCGTGGCCACATTGTGCGGGCGCTGGGGCCCCCAGGCGCTGGCGCTGG
Dd	
Db	121 GCTGCGCGCTGGCCACGTTGTGCGGGCGCTGGGGCCCCCAGGCGCTGGCGCTGG
QY	185 CGCGGACCCGCGGCGCTTTCCGCGCGCTGTGTGGCCCACTGCTGTGTGTGGCTGC
Dd	
Db	181 CGGGGACCCGCGCGCTTTTCGCGCGCTGTGTGGCCCACTGCTGTGTGTGGCTGC
QY	245 CGCACGCGCGCCCCCGCGCCCCCTCTCTTCGCCCAGGTGTCTGCTCTGAAGG
Dd	
Db	241 CGCACGCGCGCCCCCGCGCCCCCTCTTCGCCCAGGTGTCTGCTCTGAAGG
QY	305 GGCCCCAGTGTCTCAGAGCTGTGCAGCGCGCGCGGAGAACGTGCTGGCCTT
Dd	
Db	301 GGCCCCAGTGTCTCAGAGCTGTGCAGCGCGCGCGGAGAACGTGCTGGCCTT

ug-09-424-686f-9.rng

1441	GTACGGCTTCGTGTCGGGGCTGCTCGCGCGGTGCTGGTGGCCCCCAGGGCTCTCGGG	
1505	GCACAACGAACCGCGCTTCCTCAGGAAACACAAAGAAGTTTCATCTCCCTCGGGGAP	
1501	GCACAACGAACCGCGCTTCCTCAGGAAACACAAAGAAGTTTCATCTCCCTCGGGAP	
1565	CAAGCTCTCGCTGCGAGGAGCTGACGTGGAAGATGAGCTGCGGAGCATCGCGCTTC	
1561	CAAGCTCTCGCTGCGAGGAGCTGACGTGGAAGATGAGCTGCGGGGTGCGCTTC	
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1685	GGCCAAAGTTCTCTGCACCTGGCTGATGAGTGTGTACGTCTGTCGAGCTGCTCAGGTC	
1681	GGCCAAAGTTCTCTGCACCTGGCTGATGAGTGTGTACGTCTGTCGAGCTGCTCAGGTC	
1745	TTATGTCA CGGAGACA CA C G T T T C A A A G A A C A G G G C T T T T T T T C T A C C G G A A G A G	
1741	TTATGTCA CGGAGACA CA C G T T T C A A A G A A C A G G G C T T T T T T T C T A C C G G A A G A G	
1805	GAGCAAGTTGCAAGCAATTGGAAATCAGACAGCACTTTGAAGAGGGTGCAGCTCGG	
1801	GAGCAAGTTGCAAGCAATTGGAAATCAGACAGCACTTTGAAGAGGGTGCAGCTCGG	
1865	GTCGGAAGCAGAGGTCAGGCAGCATCTCGGGAAGCAGGCGCCGCCCTGCTCAGCTC	
1861	GTCGGAAGCAGAGGTCAGGCAGCATCTCGGGAAGCAGGCGCCGCCCTGCTCAGCTC	
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1921	CCGCTTCATCCCCAAGCCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGT	
1985	AGCCAGAACTTCGCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAP	
1981	AGCCAGAACTTCGCGCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAP	
2045	GTTTCAGCTGCTCAACTACAGCGGGCGCGGGCGCCCGCGCTCTCTGGGCGCTC	
2041	GTTTCAGCTGCTCAACTACAGCGGGCGCGGGCGCCCGCGCTCTCTGGGCGCTC	
2105	GGGCTCTGGACGATATCCACAGGGCCTGGGCGACCTTTCGTGCTGCGTGTGCGGG	
2101	GGGCTCTGGACGATATCCACAGGGCCTGGGCGACCTTTCGTGCTGCGTGTGCGGG	
2165	CCGCGCGCTGAGCTGTA-----	
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2189	CCAGGACAGGCTCAGCGAGGTATCGCCAGCATCATCAAAACCCAGAAACAGT	
2221	CCAGGACAGGCTCAGCGAGGTATCGCCAGCATCATCAAAACCCAGAAACAGT	
2249	CGCTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGACAGCTCCGCAAGGCCCTT	
2281	CGCTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGACAGCTCCGCAAGGCCCTT	
2309	CCACGTCTCTACCTTGA CAG A C T T C A G C C G T A C A T G C G A C A G T T C G T G G C T C A	
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2429	CAGCAGTGGCTCTTTCGACGCTCTTCTTACGCTTCATGTGCCACACAGCCGCTGCG	
2461	CAGCAGTGGCTCTTTCGACGCTCTTCTTACGCTTCATGTGCCACACAGCCGCTGCG	
2489	GGGCAAGTCTTACGTCCAGTGCCAGGGGATCCCGCAGGGGCTCCATCTCTTCCAC	

GCAAGTCTTACGTCACGTCGAGGGATCCGACGGGCTCCATCTCTCCACGCTGCT 2580
 GCAGCTGTGCTACGGGACATGAGAACAGCTGTTTGGGGATTCGGGACGG 2608
 GAGCCCTGTGCTACGGGACATGAGAACAGCTGTTTGGGGATTCGGGACGG 2640
 TGCTCCTGCGGTTTGGTGATGATTTCTTTGGTGACACCTCACCTCACCCACGGAA 2668
 TGCTCCTGCGGTTTGGTGATGATTTCTTTGGTGACACCTCACCTCACCCACGGAA 2700
 CCTTCTCAGGACCTGGTCGAGGTGCTCCTGAGTATGCTGCTGGTGAACTTGG 2728
 CCTTCTCAGGACCTGGTCGAGGTGCTCCTGAGTATGCTGCTGGTGAACTTGG 2760
 AGACAGTGGTGAACTTCTCTCTAGAACAGAGGCTGGTGCGACGCTTTTGTCTCA 2788
 AGACAGTGGTGAACTTCTCTCTAGAACAGAGGCTGGTGCGACGCTTTTGTCTCA 2820
 TGCCGGCCCAAGGCTTATTCCTCTGGTGCGGCTGCTGCTGATACCCGACCTTGA 2848
 TGCCGGCCCAAGGCTTATTCCTCTGGTGCGGCTGCTGCTGATACCCGACCTTGA 2880
 TGACAGGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAA 2908
 TGACAGGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAA 2940
 GCGGCTTCAAGGCTGGGAGGAACATGCTGCGAACTCTTTGGGGTCTTGGCGGTGAA 2968
 GCGGCTTCAAGGCTGGGAGGAACATGCTGCGAACTCTTTGGGGTCTTGGCGGTGAA 3000
 GTCAAGCTGTTTCTGGATTGAGGTGAAACAGCCCTCCAGACGGTGTGCAACCAAT 3028
 GTCAAGCTGTTTCTGGATTGAGGTGAAACAGCCCTCCAGACGGTGTGCAACCAAT 3060
 ACAGATCTCTCTGCTGAGGCTGACAGTTTCAAGCTGTCAGCTGCTGAGCTCCAT 3088
 ACAAGATCTCTCTGCTGAGGCTGACAGTTTCAAGCTGTCAGCTGCTGAGCTCCAT 3120
 ATCAGCAAGTTTGAAGAACCCCACTTTTCTGCGGCTCATCTCTGACACGCGCTC 3148
 ATCAGCAAGTTTGAAGAACCCCACTTTTCTGCGGCTCATCTCTGACACGCGCTC 3180
 TCTGCTACTCATCTCTGAAAGCCCAAGAACGAGGGATGCTGCTGGGGCCCAAGGGCG 3208
 TCTGCTACTCATCTCTGAAAGCCCAAGAACGAGGGATGCTGCTGGGGCCCAAGGGCG 3240
 CCGGCTCTGCTGCTGAGGCTGCTGAGTGGCTGCTGAGTGGCTGCTGAGTGGCTG 3268
 CCGGCTCTGCTGCTGAGGCTGCTGAGTGGCTGCTGAGTGGCTGCTGAGTGGCTG 3300
 TGACTCGACACCGTGTACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3328
 TGACTCGACACCGTGTACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
 AGCTGAGTGGAGGCTCCCGGGACGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCT 3388
 AGCTGAGTGGAGGCTCCCGGGACGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCT 3420
 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3448
 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3480
 AGAGCAGACACAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3508
 AGAGCAGACACAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3540
 CCACACCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3568
 CCACACCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3600
 GCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3628
 GCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660

QY 3629 GCTGAGTGTCCAGCACACCTGCGCTTTCACCTTCCCCACAGGCTGCGCTCGGC
 Db 3661 GCTGAGTGTCCAGCACACCTGCGCTTTCACCTTCCCCACAGGCTGCGCTCGGC
 QY 3699 CCAGGCCAGCTTTTCTCTCAACAGAGGCCGCTTCCACTCCCCACATAGGAAT
 Db 3721 CCAGGCCAGCTTTTCTCTCAACAGAGGCCGCTTCCACTCCCCACATAGGAAT
 QY 3749 TCCCCAGATTGCGCATTTTTCACCCCTGCGCTGCGCTTTCCTTTCCTTCCACCC
 Db 3781 TCCCCAGATTGCGCATTTTTCACCCCTGCGCTGCGCTTTCCTTTCCTTTCCTTCCACCC
 QY 3809 TCCAGGTGGAGACCTTCCAGAGGACCTCTGGAGCTCTCTGGAAATTTGGAGTGACC
 Db 3841 TCCAGGTGGAGACCTTCCAGAGGACCTCTGGAGCTCTCTGGAAATTTGGAGTGACC
 QY 3869 GTCCTGCTTACACAGGCGAGGACCTCTGACCTGAGATGGGGTCCCTTGGGTGCA
 Db 3901 GTGCCCTGTACACAGGCGAGGACCTCTGACCTGAGATGGGGTCCCTTGGGTGCA
 QY 3929 GGGAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTGAAA
 Db 3961 GGGAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTGAAA
 QY 3989 AAA 3991
 Db 4021 AAA 4023
 RESULT 4
 ABL53711
 ID ABL53711 standard; cDNA; 4070 BP.
 XX AC ABL53711;
 XX DT 17-JUN-2002 (first entry)
 XX Human telomerase catalytic subunit hTERT cDNA.
 XX DE Human telomerase catalytic subunit hTERT cDNA.
 XX KW hTERT; telomerase; reverse transcriptase; immortalisation; huma
 KW vaccine; enzyme; gene; ss.
 OS Homo sapiens.
 XX WO200216555-A2.
 XX PD 28-FEB-2002.
 XX PF 17-AUG-2001; 2001WO-08003726.
 XX PR 17-AUG-2000; 2000GB-00020246.
 PR 17-AUG-2000; 2000US-0225734P.
 XX PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
 XX PI Jones CU, Kipling DG, Wilkinson G, Mcsharry B, Skinner JW;
 XX WPI; 2002-315462/35.
 DR Novel hTERT-immortalized cell line (human telomerase reverse
 PT transcriptase) useful for human vaccine production and preparat
 PT antigen, such as a virus or virus-derived agent.
 PS Example 1; Fig 1; 64pp; English.
 CC The present sequence is that of hTERT cDNA in plasmid pGRN121.
 CC the catalytic subunit of human telomerase. Claimed immortalised
 CC lines for use in vaccine production are adapted to express hTERT
 CC Suitable cell lines comprise human diploid fibroblasts, e.g. MR
 CC WI38 cells, transfected with hTERT cDNA or infected by a retrov
 CC carrying hTERT cDNA, and are capable of supporting antigen prod
 CC method for preparing such cell lines using recombinant techniqu

The cell lines are also used as a diagnostic test for the
 f a virus, such as human cytomegalovirus, and to determine the
 f antiviral agents by testing the capability of a modified
 aining a reporter gene to infect the cells. The cell lines have
 f, which can be impaired in cell lines immortalised by other
 f, being able to support viral replication. The cells remain
 ally suitable for viral/vaccine cultivation

070 BP; 670 A; 1383 C; 1296 G; 721 T; 0 U; 0 Other;

98.2%; Score 3933.4; DB 6; Length 4070;

ilarity 99.1%; Pred. No. 0; Mismatches 1; Indels 36; Gaps 1;

Conservative 0; Mismatches 1; Indels 36; Gaps 1;

3GAGCGCTGCGTCTGTCGACAGTGGGAAGCCCTGGCCCGCCGACCCCGCGATG 65

CGAGCGCTGCGTCTGTCGACAGTGGGAAGCCCTGGCCCGCCGACCCCGCGATG 78

CGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGGCAGGCACTACCGGAGGTG 125

CGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGGCAGGCACTACCGGAGGTG 138

TCGCGTGGCCACGTTCTGTCGCGCGCTGGGGCCCGCAGGGCTGGCGCTGGTCAGGCG 185

TCGCGTGGCCACGTTCTGTCGCGCGCTGGGGCCCGCAGGGCTGGCGCTGGTCAGGCG 198

3GAAACCGCGCGCTTCCGCGCGTGTGGCCCGCAGTGGTGGTGGTGGTGGTGGTGGTGG 245

3GAAACCGCGCGCTTCCGCGCGTGTGGCCCGCAGTGGTGGTGGTGGTGGTGGTGGTGG 258

CAGGCG 305

CAGGCG 318

CCGAGTGTGTCAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 365

CCGAGTGTGTCAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 378

CGTGTGTGGAACGGGGCG 425

CGTGTGTGGAACGGGGCG 438

ACCTGCCAACAACGGTGTACCGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 485

ACCTGCCAACAACGGTGTACCGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 498

CCGCGTGGCGGACGAGCTGTGCTGCTTCACTGTGCGACGCTGTGCGCGCTCTTTGTGCTG 545

CCGCGTGGCGGACGAGCTGTGCTGCTTCACTGTGCGACGCTGTGCGCGCTCTTTGTGCTG 558

TGCTCCAGCTGCGCTACAGAGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 605

TGCTCCAGCTGCGCTACAGAGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 618

TCAGCG 665

TCAGCG 678

CTGGAACCAATAGCGTCAGGAGCGCGGGGTCCCGCTGGGCGCTGCCAGCGCGCGGGTGGC 725

CTGGAACCAATAGCGTCAGGAGCGCGGGGTCCCGCTGGGCGCTGCCAGCGCGCGGGTGGC 738

3GAGCGCGGGGGAGTGCAGCGAAGTCTGCGGTGGCCCAAGAGGCCCGCGCGGTGGC 785

3GAGCGCGGGGGAGTGCAGCGAAGTCTGCGGTGGCCCAAGAGGCCCGCGCGGTGGC 798

TCGCGCTGAGCGGAGCGAGCGCGCGCTGGGCGAGGGTCTGGGCGCGCGCGCGCGCGCG 845

TCGCGCTGAGCGGAGCGAGCGCGCGCTGGGCGAGGGTCTGGGCGCGCGCGCGCGCGCG 858

CGCTTATATCCCAAGCTGACGGGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 905

CGCTTATATCCCAAGCTGACGGGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 918

906 GCCACCTCTTTGGAGGTGGCTCTCTGGCAGCGGCCACTCCACCCATCCGT

919 GCCACCTCTTTGGAGGTGGCTCTCTGGCAGCGGCCACTCCACCCATCCGT

966 CAGCACACAGCGGGCGGCCCATTCACATCGGGGCGACACATCTCCCTGGGACAC

979 CAGCACACAGCGGGCGGCCCATTCACATCGGGGCGACACATCTCCCTGGGACAC

1026 CCCCCTGGTGTACCGGAGACCAAGCACTTCTCTACTCTCTCAGGCGCAAGGA

1039 CCCCCTGGTGTACCGGAGACCAAGCACTTCTCTACTCTCTCAGGCGCAAGGA

1086 CGGCTCTCTTCTCTACTCTCTCTGAGGCCAGCCTGACTGCGGCTTCGGAG

1099 CGGCTCTCTTCTCTACTCTCTCTGAGGCCAGCCTGACTGCGGCTTCGGAG

1146 GAGACCACTTCTCTGGGTTCAGGCGCTTGGATGCGAGGCACTCCCGCAGGT

1159 GAGACCACTTCTCTGGGTTCAGGCGCTTGGATGCGAGGCACTCCCGCAGGT

1206 CTGCCCCAGCGCTACTTGGCAATGCGGCCCTCTCTCTGGAGCTCTTGGGAA

1219 CTGCCCCAGCGCTACTTGGCAATGCGGCCCTCTCTCTGGAGCTCTTGGGAA

1266 CAGTGCCCTACCGGGTGTCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGGT

1279 CAGTGCCCTACCGGGTGTCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGGT

1326 GCAGCGGTGTCTGTGCGGGGAGAAAGCCCGAGGGCTCTGTGGCGGCGCCCGA

1339 GCAGCGGTGTCTGTGCGGGGAGAAAGCCCGAGGGCTCTGTGGCGGCGCCCGA

1386 GACACAGACCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

1399 GACACAGACCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

1446 TACGGCTCTGCTGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

1459 TACGGCTCTGCTGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

1506 CACAAACAAACCGCGCTTCTCTCAGGAAACCAAGAAAGTTCATCTCTCTGGGAA

1519 CACAAACAAACCGCGCTTCTCTCAGGAAACCAAGAAAGTTCATCTCTCTGGGAA

1566 AAGCTCTGCTGCGAGGCTGACGCTGGAAGATGAGCGTGGGAGCTGGCTTG

1579 AAGCTCTGCTGCGAGGCTGACGCTGGAAGATGAGCGTGGGAGCTGGCTTG

1626 AGGAGCCAGGGGTGGCTGTGTTCCGGCCGAGAGCAACCGTCTGCGGTGAGGA

1639 AGGAGCCAGGGGTGGCTGTGTTCCGGCCGAGAGCAACCGTCTGCGGTGAGGA

1686 GCCAAGTTCCTGCACTGGCTGTGAGTGTGTAAGTCTGAGCTGCTCAGGTC

1699 GCCAAGTTCCTGCACTGGCTGTGAGTGTGTAAGTCTGAGCTGCTCAGGTC

1746 TATGTACCGAGAGCAAGTTCCTGGAAGAACAGGCTCTTTTCTACCCGGAAGAG

1759 TATGTACCGAGAGCAAGTTCCTGGAAGAACAGGCTCTTTTCTACCCGGAAGAG

1806 AGCAAGTTCGAAAGCAATGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCG

1819 AGCAAGTTCGAAAGCAATGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCG

1866 TCGAAGCAGAGTTCAGGAGCATTCGGGAAGCAAGCCCGCCCTGCTGAGAGTCTC

1879 TCGAAGCAGAGTTCAGGAGCATTCGGGAAGCAAGCCCGCCCTGCTGAGAGTCTC

1926 CGCTTATATCCCAAGCTGACGGGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG

1939 CGCTTATATCCCAAGCTGACGGGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG

CGAAGCGTTC	CGCAGAGAAAGAGGGCCGAGCGTCTCACTCTGAGGGTGAAGGCATCTG	2045
CGAAGCGTTC	CGCAGAGAAAGAGGGCCGAGCGTCTCACTCTGAGGGTGAAGGCATCTG	2058
CGAGCGTCTCA	CTACGAGCGGGCGGGCCCGCGCTCTCTGGCGCCTCTGCGCTCTGTCGTG	2105
CGAGGTGCTCA	CTACGAGCGGGCGGGCCCGCGCTCTCTGGCGCCTCTGCGCTCTGTCGTG	2118
CGTGACGATAT	CCACAGGGCCCTGGCGCACCTTCGTGCTGCTGTGCGGGCCCAAGGAC	2165
CGTGACGATAT	CCACAGGGCCCTGGCGCACCTTCGTGCTGCTGTGCGGGCCCAAGGAC	2178
CGCGCTGAGCTGA	-----CATCCCC	2189
CGCGCTGAGCTGA	CTTTGTCAAGGTGGATGTGACGGGGCGGTACGACACCATCCCC	2238
GGACAGGCTCA	CGAGAGTCAATCGCAGCATCATCAAAACCCAGAAACAGTACTGCGTG	2249
GGACAGGCTCA	CGAGAGTCAATCGCAGCATCATCAAAACCCAGAAACAGTACTGCGTG	2298
TCGGTATGCCGT	GTCCAGAAAGCGGCCATGGGCAAGTCCGCAAGGCCTTCAAGAGC	2309
TCGGTATGCCGT	GTCCAGAAAGCGGCCATGGGCAAGTCCGCAAGGCCTTCAAGAGC	2358
AGCTCTCTAC	CTTGACAGACTCCAGCCGTACATCGCAGTTCGTGGCTCACCTGCAG	2369
AGCTCTCTAC	CTTGACAGACTCCAGCCGTACATCGCAGTTCGTGGCTCACCTGCAG	2418
AGACCGCGCTC	GAGGATCGCTCATCGAGCAGTCTCCTCCGTGAATGAGGC	2429
AGACCGCGCTC	GAGGATCGCTCATCGAGCAGTCTCCTCCGTGAATGAGGC	2478
CGAGTGCCTCT	TCGACGTCTTCAAGTTCATGTGCCACACACCGCTGGCGATCAGG	2489
CGAGTGCCTCT	TCGACGTCTTCAAGTTCATGTGCCACACACCGCTGGCGATCAGG	2538
CGAGTCTTAC	GTCCAGGGGATCCGCGAGGCTCCATCTCTCCACGCTGCTC	2549
CGAGTCTTAC	GTCCAGGGGATCCGCGAGGCTCCATCTCTCCACGCTGCTC	2598
CGAGCTGTCTA	CGGCGACATGAGAACAGCTGTTTGGGGGATTCGCGGGAGCGG	2609
CGAGCTGTCTA	CGGCGACATGAGAACAGCTGTTTGGGGGATTCGCGGGAGCGG	2658
CGCTCTCGCT	TTGGTGATTTCTTTGGTGACACCTCACCTCACCCACGCGAAA	2669
CGCTCTCGCT	TTGGTGATTTCTTTGGTGACACCTCACCTCACCCACGCGAAA	2718
CTTCTCTCAGA	CCCTGGTCGAGTGTCCGTGAGTATGGCTGGGTGGAATCTGCGG	2729
CTTCTCTCAGA	CCCTGGTCGAGTGTCCGTGAGTATGGCTGGGTGGAATCTGCGG	2778
GACAGGTGTGA	CTTCCCTGTAGAACAGAGCCCTGGGTGGCACGCGTTTGTTCAG	2789
GACAGGTGTGA	CTTCCCTGTAGAACAGAGCCCTGGGTGGCACGCGTTTGTTCAG	2838
CGCGGCCAC	CGGCTATTCCTGTGGCGCTGCTGGATACCCGACCCCTGGAG	2849
CGCGGCCAC	CGGCTATTCCTGTGGCGCTGCTGGATACCCGACCCCTGGAG	2898
CGAGAGCGACT	ATCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACTTCAAC	2909
CGAGAGCGACT	ATCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACTTCAAC	2958
CGGCTTCAAG	GGTGGAGNACATGCTTCGCAACTCTTTGGGGTCTTGGCGGTGAAG	2969
CGGCTTCAAG	GGTGGAGNACATGCTTCGCAACTCTTTGGGGTCTTGGCGGTGAAG	3018
TCACAGCTGT	TTCTGATTTGAGGTGAACGCTCCAGACCGTGTGCACCAACATC	3029
TCACAGCTGT	TTCTGATTTGAGGTGAACGCTCCAGACCGTGTGCACCAACATC	3078
CAAGATCCCT	CTGCTCAGCGGTACAGGTTTTCACGATGTGTCTGCAGCTCCCATTT	3089

Db	3079	TACAGAGTCTCTCTGCTGCGAGGGGTACAGGTTTACGCATGTGTGCTGCGAGCT
Qy	3090	CATCAGCAAGTTTGGAAAGACCCACACATTTTCTCTGCGCGTCACTCTCTGACAC
Db	3139	CATCAGCAAGTTTGGAAAGACCCACACATTTTCTCTGCGGTCACTCTCTGACAC
Qy	3150	CTCTGCTACTCCATCTCTGAAAGCCAGAACGACGAGGATGTCTGCTGGGGGCCAA
Db	3199	CTCTGCTACTCCATCTCTGAAAGCCAGAACGACGAGGATGTCTGCTGGGGGCCAA
Qy	3210	GCCGGCCCTCTGCCCTCCGAGGGCCGTGAGTGGCTGTGCCACCAAGCAATTCCTT
Db	3259	GCCGGCCCTCTGCCCTCCGAGGGCCGTGAGTGGCTGTGCCACCAAGCAATTCCTT
Qy	3270	CTGACTCGACACCGTGTCACTACGTGCCACTCTCTGGGGTCACTTCAGGACAGCG
Db	3319	CTGACTCGACACCGTGTCACTACGTGCCACTCTCTGGGGTCACTTCAGGACAGCG
Qy	3330	CAGCTGAGTGGAAAGCTCCGGGGAGACGCGTGACTGCTCCTTGGAGGCGCGAGCG
Db	3379	CAGCTGAGTGGAAAGCTCCGGGGAGACGCGTGACTGCTCCTTGGAGGCGCGAGCG
Qy	3390	GCATGCGCCTCAGACTTCAAGACCATCTTGACTGATGGCCACCCGCCACACAG
Db	3439	GCATGCGCCTCAGACTTCAAGACCATCTTGACTGATGGCCACCCGCCACACAG
Qy	3450	GAGAGCAGACACAGCAGCCCTGTACGCCGGGCTTACGTCCACAGGGAGGGAA
Db	3499	GAGAGCAGACACAGCAGCCCTGTACGCCGGGCTTACGTCCACAGGGAGGGAA
Qy	3510	CCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCGTGAGTGGTGTGTGGCG
Db	3559	CCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCGTGAGTGGTGTGTGGCG
Qy	3570	TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGGCTCAGCGAGTGTCCAG
Db	3619	TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGGCTGAGCGAGTGTCCAG
Qy	3630	CTGAGTGTCCAGCACACTGCGGCTTTCATTTCCCA CAGGCTGGGCGCTCGGC
Db	3679	CTGAGTGTCCAGCACACTGCGGCTTTCATTTCCCA CAGGCTGGGCGCTCGGC
Qy	3690	CAGGGCCAGCTTTTCTTCA CAGAGGCCCGGCTTCCACTCCCACTAGGAT
Db	3739	CAGGGCCAGCTTTTCTTCA CAGAGGCCCGGCTTCCACTCCCACTAGGAT
Qy	3750	CCCCAGATTGGCCATTGTTCACCCCTCGCCCTGCCCCCTTTGCCCTTCCACCC
Db	3799	CCCCAGATTGGCCATTGTTCACCCCTCGCCCTGCCCCCTTTGCCCTTCCACCC
Qy	3810	CCAGGTGGAGCCCTTGAGAAAGACCCCTGGGAGCTCTGGGAAATTTGGAGTGACCG
Db	3859	CCAGGTGGAGCCCTTGAGAAAGACCCCTGGGAGCTCTGGGAAATTTGGAGTGACCG
Qy	3870	TGCCCTGTACACAGGCGAGACCTTGACACTGGATGGGGGTCCCTGTGGGGTCA
Db	3919	TGCCCTGTACACAGGCGAGACCTTGACACTGGATGGGGGTCCCTGTGGGGTCA
Qy	3930	GGGAGGTGCTGTGGGAGTAAAACTAGAAATATATGAGTTTTTTCAGTTTTTCAAA
Db	3979	GGGAGGTGCTGTGGGAGTAAAACTAGAAATATATGAGTTTTTTCAGTTTTTCAAA

RESULT 5	
AAZ00724	
ID	AAZ00724 standard; DNA; 4015 BP.
XX	
XX	
XX	AAZ00724;
XX	
XX	
DT	06-OCT-1999 (first entry)
XX	
XX	Human telomerase catalytic domain
DE	

· catalytic domain; human; quantitation; tumour cell; melanoma; metastases; T-cell lymphoblastoma; chronic myeloid leukemia; atic leukemia; melanoma; pulmonary carcinoma; colon cancer; er; ss.

18.

-A1.

3.

3: 98DE-01004372.

3: 98DE-01004372.

M M W.

131408/37.

in tumor cells by amplifying mRNA encoding the catalytic subunit of p34^{cdc2}.

-g 1A-B; 26pp; German.

tion describes a novel method for the quantitation of tumour body fluid which comprises (1) enrichment or isolation of α -fetoprotein in the sample, (2) amplification of mRNA from these cells by reverse transcription polymerase chain reaction (RT-PCR) using the catalytic subunit of telomerase and (3) quantifying the amplified mRNA. The method is applied to tumour cells derived from various human tumours, e.g. associated with a wide range of tumours such as glioblastoma, chronic myeloid or acute lymphatic leukaemia, lung adenocarcinoma, cancer of colon or breast etc. This method can be used to detect telomerase activity in body fluids and to code a human telomerase protein catalytic domain.

)15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

98.2%; Score 3933; DB 2; Length 4015;

ilarity 99.1%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 36; Gaps 1;

'AGCGCTGCGTCCTGTGCGCACGTGGAGCCCTGGCCCCGGCCACCCCGGATGCC 67

'AGCGCTGCGTCCTGTGCGCACGTGGAGCCCTGGCCCCGGCCACCCCCGATGCC 60

12'GGGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGAGCCACTACCGGAGGTGCT

'GGGCTCCCCGGTGGCGAGCCGTGGCTCCCTGCTGGCGAGCCACTACCGCGAGGTGCT 12

'CGCTGGCCACGTTCGTGGCGGCCCTGGGGCCCAAGGCTGGCTGGTGCAGCGCG 18'

CGCTGGCCACGTTTCGTGGCGCGCTGGGGCCCAAGGCTGGCGCTGGTGCAGCGCG 180

!ACCGCGCGCTTTCCGCGCGCTGGTGGCCCAAGTGCCTGGTGTGCGTGCCCTGGGACGC 247

!ACCCGGCGGCTTTCGGCGGCTGGTGGCCAGTGCCCTGGTGTGCTGGGACGC 240

:GGCGGCCCCCGCGGCCCTCCTTCGCCAGGTGCTCTGCCTGAAGAGCTGGTGGC 307

'GGCGGCCCCCGCGCGCCCTCCTTCGGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC 300

5'-GAGTGTGCAGAGGCTGTGCGAGCGCGGCGAAGAACGTGCTGGCCTTCGGCTTCGC-3'

5'-GAGTGTGTCAGAGGCTGTGCGAGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC 360

5'-TGTCTGGACGGGGGCCCCCGGGGGCCCCCGAGGCCCTTACACCAACGAGGTGGCAGCTA 427

TGCTGGACGGGGCCCCGGGGGGCCCCCGAGGGCCTTCACCAACAGCGTGCGCAGCTA 420

5'-TGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCTGCTGCTGCG 487

421	DB	CCTGCCAAACACGGTGAACCGAGACACTGTGGGGGAGCGGGGCGGTGGGGGCTGGTGG
488	QY	CCGGTGGGGACACGCTGCTGGTTCACTCTGTCGGCACGTCGTCGCGCTCTTTTG
481	DB	CCGGTGGGGACACGCTGCTGGTTCACTCTGTCGGCACGTCGTCGCGCTCTTTTG
548	QY	GGCTCCAGCTTGGCGCTTACAGGTGTGGGGCGCGCGCTGTGTACAGATTGGCG
541	DB	GGCTCCAGCTTGGCGCTTACAGGTGTGGGGCGCGCGCTGTGTACAGATTGGCG
608	QY	TCAGGCCGGCCCCCGGCACACGCTAGTGTGACCCCGGAAGGCTGTGGATGCG
601	DB	TCAGGCCGGCCCCCGGCACACGCTAGTGTGACCCCGGAAGGCTGTGGATGCG
668	QY	CTGGAACCATAGCGTCAAGGAGGCGGGGTCCCCCTGGGCTGCGACGCCCGG
661	DB	CTGGAACCATAGCGTCAAGGAGGCGGGGTCCCCCTGGGCTGCGACGCCCGG
728	QY	GAGGCGGGGGAGTGTGCAGCCGAAGTCTGCGGTTGCCCAAGAGGCCCAAGGC
721	DB	GAGGCGGGGGAGTGTGCAGCCGAAGTCTGCGGTTGCCCAAGAGGCCCAAGGC
788	QY	TGCCCTTGAGCCGAGCGGAGCGCCGTTGGCAGGGGTCTTGGGCCCAACCGG
781	DB	TGCCCTTGAGCCGAGCGGAGCGCCGTTGGCAGGGGTCTTGGGCCCAACCGG
848	QY	CGGTGACCCGAGTGACCGTGGTTCTTGTGTGGTGTACCTGCGCAGACCCCGCG
841	DB	CGGTGACCCGAGTGACCGTGGTTCTTGTGTGGTGTACCTGCGCAGACCCCGCG
908	QY	CACCTCTTTGAGGGTGGCTCTCTGCGACGGCGCACTGCCAACCACTCCGTGG
901	DB	CACCTCTTTGAGGGTGGCTCTCTGCGACGGCGCACTGCCAACCACTCCGTGG
968	QY	GCACACGGGGCCCCCATCTCCATCGCGGGCCACGACGTCCTGGGACACGC
961	DB	GCACACGGGGCCCCCATCTCCATCGCGGGCCACGACGTCCTGGGACACGC
1028	QY	CCCCGTGTAGCCGAGACCAAGCACTTCTCTACTCTCTCAGGGGACAAAGGAGC
1021	DB	CCCCGTGTAGCCGAGACCAAGCACTTCTCTACTCTCTCAGGGGACAAAGGAGC
1088	QY	GCCCTCTCTACTCTAGCTCTCTGAGGCCACGCTGACTGGGCTCGGAGGC
1081	DB	GCCCTCTCTACTCTAGCTCTCTGAGGCCACGCTGACTGGGCTCGGAGGC
1148	QY	GACCATCTTTCTGGTTTCAGGCCCTGGATGCCAGGACTCCCCGCAAGTTGC
1141	DB	GACCATCTTTCTGGTTTCAGGCCCTGGATGCCAGGACTCCCCGCAAGTTGC
1208	QY	GCCCCAGCGTACTTGGCAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAAC
1201	DB	GCCCCAGCGTACTTGGCAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAAC
1268	QY	GTGCCCCCTACGGGTGTCTCTCAAGACGCACTGCCCGCTCGAGCTCGGTCA
1261	DB	GTGCCCCCTACGGGTGTCTCTCAAGACGCACTGCCCGCTCGAGCTCGGTCA
1328	QY	AGCCGTGTCTGTGCCCGGAGAGCCCCAGGGCTGTGTGGCGGCCCGGAGG
1321	DB	AGCCGTGTCTGTGCCCGGAGAGCCCCAGGGCTGTGTGGCGGCCCGGAGG
1388	QY	CACAGACCCCGTGGCTGTGAGCTGTCTCCGACGACACGACGACCCCTGGC
1381	DB	CACAGACCCCGTGGCTGTGAGCTGTCTCCGACGACACGACGACCCCTGGC
1448	QY	CGGCTTGTGTGGGCGCTGCTGTGCGCGGCTGTGTGCCCCAGGGCTCTGGGGCT
1441	DB	CGGCTTGTGTGGGCGCTGCTGTGCGCGGCTGTGTGCCCCAGGGCTCTGGGGCT
1508	QY	CAACGAACCGGCTTCTCTCAGGAACACCAAGAAATTCATCTCCCTGGGGAAGC
1501	DB	CAACGAACCGGCTTCTCTCAGGAACACCAAGAAATTCATCTCCCTGGGGAAGC

QY	2612	GCTCCTCGGTTTGGTGGATCAATTTCTTTGTTGGTGACACTCACTGACCCACG	
Db	2641	GCTCCTCGGTTTGGTGGATCAATTTCTTTGTTGGTGACACTCACTGACCCACG	
QY	2672	CTTCTCCAGGACCTCGTCCGAGGTGTCCCTGAGTATGGCTGGGTGGACGGCTTTTG	
Db	2701	CTTCTCCAGGACCTCGTCCGAGGTGTCCCTGAGTATGGCTGGGTGGTGAAT	
QY	2732	GACAGTGGTGAATTTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGCTTTTG	
Db	2761	GACAGTGGTGAATTTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGCTTTTG	
QY	2792	GCCGGCCACGGCTATTTCCTGTGTGCGGCTGCTGCTGGATACCCGGACCC	
Db	2821	GCCGGCCACGGCTATTTCCTGTGTGCGGCTGCTGCTGGATACCCGGACCC	
QY	2852	GCAGAGGACATACTCAGACTATGCCGGACCTCCATCAGAGCCAGTCTCACCT	
Db	2881	GCAGAGGACATACTCAGACTATGCCGGACCTCCATCAGAGCCAGTCTCACCT	
QY	2912	CGGCTTCAAGGCTGGAGGAACAATGGTCGCAAACTCTTTGGGCTCTTGGCGC	
Db	2941	CGGCTTCAAGGCTGGAGGACAAATGGTCGCAAACTCTTTGGGCTCTTGGCGC	
QY	2972	TCACAGCCTGTTTCTGGATTTGAGGTGAGTGAAACAGCTCCAGACGGTGTGACCA	
Db	3001	TCACAGCCTGTTTCTGGATTTGAGGTGAAACAGCTCCAGACGGTGTGACCA	
QY	3032	CAGATCTCCTGCTCGAGCGTACAGGTTTCAAGCATGTGTCTGCAGCTCTCC	
Db	3061	CAGATCTCCTGCTCGAGCGTACAGGTTTCAAGCATGTGTCTGCAGCTCTCC	
QY	3092	TCACGAAGTTTGAAGAAACCCACATTTTCTGCGCGTCACTCTGACACGGI	
Db	3121	TCACGAAGTTTGAAGAAACCCACATTTTCTGCGCGTCACTCTGACACGGI	
QY	3152	CTGCTACTCCATCTGAAAGCCAGAAACGAGGGATGTGCTGGGGGCCAAGG	
Db	3181	CTGCTACTCCATCTGAAAGCCAGAAACGAGGGATGTGCTGGGGGCCAAGG	
QY	3212	CGGCCCCTCTGCCCTCCGAGCGCTGCAGTGGCTGTGCCACCAAGCATTCCTGC	
Db	3241	CGGCCCCTCTGCCCTCCGAGCGCTGCAGTGGCTGTGCCACCAAGCATTCCTGC	
QY	3272	GACTCGACACCGGTGCACTTACGTGCCACTCTCTGGGGTCACTCAGACAGCCCI	
Db	3301	GACTCGACACCGGTGCACTTACGTGCCACTCTCTGGGGTCACTCAGACAGCCCI	
QY	3332	GCTGAGTCCGAGACTCCCGGGGACGACGTGACTGCCCTGGAGGCCGACGCCAI	
Db	3361	GCTGAGTCCGAGACTCCCGGGGACGACGTGACTGCCCTGGAGGCCGACGCCAI	
QY	3392	ACTGCCCTCAGACTTCAAGACCACTCTGGACTGATGGCCACCCGCCCAACGCCCI	
Db	3421	ACTGCCCTCAGACTTCAAGACCACTCTCTGACTGATGGCCACCCGCCCAACGCCCI	
QY	3452	GAGCAGACCCAGCAGCCCTGTGACGCCGGCTCTACGTCCAGGGAGGGAGG	
Db	3481	GAGCAGACCCAGCAGCCCTGTGACGCCGGCTCTACGTCCAGGGAGGGAGG	
QY	3512	CACACCAGGCCCGCACCGCTGGAGTCTGAGGCCCTGAGTGTGTTGGCCGG	
Db	3541	CACACCAGGCCCGCACCGCTGGAGTCTGAGGCCCTGAGTGTGTTGGCCGG	
QY	3572	CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCFI	
Db	3601	CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCFI	
QY	3632	GAGTGTCCAGCACACTGCGCGTCTTCACTTCCCCACAGCTGGCGCTCGGCTC	
Db	3661	GAGTGTCCAGCACACTGCGCGTCTTCACTTCCCCACAGCTGGCGCTCGGCTC	
QY	3692	GGGCCAGCTTTTCTCCACACAGGAGCCCGGCTTCCACTCCCCCAATAGGAATAGFI	

|||||
 ACCAGCTTTCTCACCAGGAGCGGCTTCACTCCCAATAGGAATATCCATCC 3780
 AGATTGCGCATTTTACCCCTCGCCCTGCTTCTTTCCTTCCACCCCAACCATCC 3811
 AGATTGCGCATTTTACCCCTCGCCCTGCTTCTTTCCTTCCACCCCAACCATCC 3840
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 AGTGTGTGGGAGTAAATATCTGATATATATGATGATTTTTCAGTTTGAATAAAA 3986
 GGTGTGTGGGAGTAAATATCTGATATATATGATGATTTTTCAGTTTGAATAAAA 4015

andard; cDNA; 4015 BP.

(first entry)

erase reverse transcriptase (hTERT) cDNA.

reverse transcriptase; human; hTERT; cell proliferation;

is.

Location/Qualifiers
 56..3454
 /*tag= a

2.

99MO-US007097.
 98US-00052864.
 98US-00128354.

ON CORP.

10842/52.
 32090.

ic polypeptide and polynucleotide, useful for increasing
 ctivity in a cell.

Fig 2; 24pp; English.

nucleotide sequence of cDNA encoding human telomerase reverse
 se (hTERT, see AAY32090). Human telomerase is a target for
 and treating diseases relating to cell proliferation and
 such as cancer, or for increasing the proliferative capacity
 A claimed method for increasing the proliferative capacity of
 e cell, especially a human or other mammalian cell, involves
 into the cell a recombinant hTERT polynucleotide encoding an
 it in which residues 192-323, 200-323, 192-271, 200-271, 222-
 0, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A
 hod for reducing telomerase activity in a cell involves
 a recombinant polynucleotide encoding a hTERT variant having
 of amino acids 192-450, 560-565, 637-660, 748-764 or
 The polynucleotides are obtained by mutagenesis of the hTERT

CC coding sequence
 XX
 SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
 Query Match 98.2%; Score 3933; DB 2; Length 4015;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 3979; Conservative 0; Mismatches 0; Indels 36;
 QY 8 GCAGCGCTGCTCTCTGCGCACGTGGGAAGCCCTGGGCCCGCCACCCCGG
 Db 1 GCAGCGCTGCTCTCTGCGCACGTGGGAAGCCCTGGGCCCGCCACCCCGG
 QY 68 GCGCGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCTGCGGAGCCTACCGCG
 Db 61 GCGCGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCTGCGGAGCCTACCGCG
 QY 128 GCGCGCTGCGCACGTTCGTCGCGGCGCTGGGGCCCGCAGGGCTGGCGTGTGTG
 Db 121 GCGCGCTGCGCACGTTCGTCGCGGCGCTGGGGCCCGCAGGGCTGGCGTGTGTG
 QY 188 GGAACCGCGCGCTTTCGCGCGCTGCTGGCCAGTGCCTGCTGTGTGCTGCTG
 Db 181 GGAACCGCGCGCTTTCGCGCGCTGCTGGCCAGTGCCTGCTGTGTGCTGCTG
 QY 248 AGGCG
 Db 241 AGGCG
 QY 308 CGGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG
 Db 301 CGGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG
 QY 368 GTGCTGCGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 Db 361 GTGCTGCGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 QY 428 CTTGCCCAACACGCTGACCGACGACACTGCGGGGGAGCGGGGGCTGGGGCTGCT
 Db 421 CTTGCCCAACACGCTGACCGACGACACTGCGGGGGAGCGGGGGCTGGGGCTGCT
 QY 488 CGCGTGGCGGAGCGAGCTGTGTTTCACTGCTGGCAGCTGCGCGCTCTTTTCT
 Db 481 CGCGTGGCGGAGCGAGCTGTGTTTCACTGCTGGCAGCTGCGCGCTCTTTTCT
 QY 548 GGTCTCCAGCTGCGCTTACAGTGTGCGGGCGCGCGCTGTACCACTCGGCG
 Db 541 GGTCTCCAGCTGCGCTTACAGTGTGCGGGCGCGCGCTGTACCACTCGGCG
 QY 608 TCAGGCG
 Db 601 TCAGGCG
 QY 668 CTGGAACCATAGCTCAGGAGCGCGGGGTCCCGCTGGGCGCTGCCAGCCCCCGG
 Db 661 CTGGAACCATAGCTCAGGAGCGCGGGGTCCCGCTGGGCGCTGCCAGCCCCCGG
 QY 728 GAGGCGCGGGGCGAGTGCAGCGCGAAGTCTGCGGTTTGCCCAAGAGGCCCGAGG
 Db 721 GAGGCGCGGGGCGAGTGCAGCGCGAAGTCTGCGGTTTGCCCAAGAGGCCCGAGG
 QY 788 TCGCCCTTGAGCGGAGCGGAGCGCGCGCTTGGGCGAGGGGTCTGGGCCCGCCCGG
 Db 781 TCGCCCTTGAGCGGAGCGGAGCGCGCGCTTGGGCGAGGGGTCTGGGCCCGCCCGG
 QY 848 GGTGACCGAGTGTGACCGGTGTTTCTGTGTGTGTGTCACTGCCAGACCGCGCG
 Db 841 GGTGACCGAGTGTGACCGGTGTTTCTGTGTGTGTGTCACTGCCAGACCGCGCG
 QY 908 CACCTCTTTGGAGGGTGGCGCTCTCTGGCAGCGCGCGCGCGCGCGCGCGCGCG
 Db 901 CACCTCTTTGGAGGGTGGCGCTCTCTGGCAGCGCGCGCGCGCGCGCGCGCGCG
 QY 968 GCACACACGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG

tandard; cDNA; 4015 BP.

0 (first entry)
ing a human telomerase reverse transcriptase (TERT).
omerase reverse transcriptase; TERT; T lymphocyte activation;
cell; telomerase activity; cancer cell; proliferating cell;
cal destruction; telomerase; cancer; proliferation disease; ss.
ns.

XX	Key	Location/Qualifiers
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FT		/product= "telomerase reverse transcriptase"
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XX	W09950392-A1.	
XX		
PD	07-OCT-1999.	
XX		
PF	30-MAR-1999;	99WO-US006898.
XX		
PR	31-MAR-1998;	98US-0112006P.
XX		
PA	(GERO-) GERON CORP.	
XX		
PI	Gaeta FCA;	
XX		
DR	WPI; 1999-610845/52.	
DR	P-PSDB; AAY43621.	
XX		
PT	Eliciting an in vivo immune response for prevention and treatment of	
PT	cancers.	
XX		
PS	Disclosure; Fig 2; 26pp; English.	
XX		
CC	The present sequence encodes a human telomerase reverse transcriptase (TERT) polypeptide. The protein is used in the method of the invention for	
CC	The specification describes a method for activating a T lymphocyte comprising contacting the T lymphocyte with a dendritic cell that expresses a TIR peptide in the context of a MHC class I or MHC class II molecule. The protein causes induction of an in vivo immunologic response to telomerase activity. Cancer cells are characterized by overexpression of endogenous TERT gene and the presence of detectable telomerase activity. Therefore, by eliciting a specific immune response to TERT or to TERT-expressing cells, it is possible to select and proliferate cells for immunological destruction. The method of the invention for eliciting an in vivo immune response to telomerase by activating a T lymphocyte, and is useful for prevention and treatment of cancer and other proliferation diseases/conditions	
XX		
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;	
Query Match		
Best Local Similarity 99.1%; Score 3933; DB 2; Length 4015;		
Matches 3979; Conservative 0; Mismatches 0; Indels 36;		
QY	8	GCAGCGCTGCCGTCTGCTGGCGCAGTGGGAGAGCCCTGGCCCGCGCCACACCCCGG
Db	1	GCAGCGCTGCCGTCTGCTGGCGCAGTGGGAGAGCCCTGGCCCGCGCCACACCCCGG
QY	68	GCAGCGCTGCCGTGCCGAGCCGTGGCTCCCTGCTGGCAGCCACTACACGCGCG
Db	61	GCAGCGCTGCCGTGGCGAGCCGTGGCTCCCTGCTGGCAGCAGCACTACACGCGCG
QY	128	GCAGCGTGGCCACATTCTGGTGGCGCCCTGGGAGCCCGCCAGGGCTGGCGGTGGTGC
Db	121	GCAGCGTGGCCACATTCTGGTGGCGCCCTGGGAGCCCGCCAGGGCTGGCGGTGGTGC
QY	188	GGACCCGGCGGCTTTTCGGCGCGCTGGTGGGCCCAAGTGCCTGGTGGCGTGGCTCT
Db	181	GGACCCGGCGGCTTTTCGGCGCGCTGGTGGGCCCAAGTGCCTGGTGGCGTGGCTCT
QY	248	ACGGCGCGCCCGCCCGCGCCCTCCCTCCCTCCGCCAGGTGTCTGCTCTGAAGAGAG
Db	241	ACGGCGCGCCCGCCCGCGCCCTCCCTCCCTCCGCCAGGTGTCTGCTCTGAAGAGAG
QY	308	CCGAGTGTCTCAGAGGCTGTGGCGCGCGCGCGCGAAGAACGTGCTGTGCGCTTCG
Db	301	CCGAGTGTCTCAGAGGCTGTGGCGCGCGCGCGAAGAACGTGCTGTGCGCTTCG
QY	368	GCTGTGTGACGGGGCCCGCGGGGCGCCCGGAGGCGCTTTCACACCAGCGTGG

QY	1508	CAACGAAGCGCGCTTCTCTCAGGAACACCAAGAGTTTCACTCCCTCGGGGAAGG
DB	1501	CAACGAACGGCGCTTCTCTCAGGAACACCAAGAGTTTCACTCCCTCGGGGAAGC
QY	1568	GCTCTCGCTGCAGGAGCTGACGTGGGAAGATGAGCGTCGGGACATGCCCTCTGGG
DB	1561	GCTCTCGCTGCAGGAGCTGACGTGGGAAGATGAGCGTCGGGAATGCGCCTTGGC
QY	1628	GAGCCCAAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAGGAGA
DB	1621	GAGCCCAAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAGGAGA
QY	1688	CAAGTTCCTGCACCTGGCTGATGAGTGTGATCGTCGACGCTGCTCAGTCTTT
DB	1681	CAAGTTCCTGCACCTGGCTGATGAGTGTGATCGTCGACGCTGCTCAGTCTTT
QY	1748	TGTCACGGAGACACGCTTTCAAAAGAACAGCTCTTTTCTACCGGAAGAGTG
DB	1741	TGTCACGGAGACACGCTTTCAAAAGAACAGCTCTTTTCTACCGGAAGAGTG
QY	1808	CAAGTTCGAAGCANTGGAATCAGACAGCACTTGAAGAGGGTGACGCTCGGGG
DB	1801	CAAGTTCGAAGCANTGGAATCAGACAGCACTTGAAGAGGGTGACGCTCGGGG
QY	1868	GGAAGCAGAGGTCAGGCAGCATCGGAGNACAGGCCCGCCCTGCTGACGTCCA
DB	1861	GGAAGCAGAGGTCAGGCAGCATCGGAGNACAGGCCCGCCCTGCTGACGTCCA
QY	1928	CTTTCATCCCAAGCCTCAGCGGCTGCGGCCGATTGTGAACATGACATACGTCG
DB	1921	CTTTCATCCCAAGCCTCAGCGGCTGCGGCCGATTGTGAACATGACATACGTCG
QY	1988	CAGAACGTTTCGCGAGAGAAAGAGGCGCAGCGCTCTCACCTCAGGGGTGAAGG
DB	1981	CAGAACGTTTCGCGAGAGAAAGAGGCGCAGCGCTCTCACCTCAGGGGTGAAGG
QY	2048	CAGGCTGCTCAACTACGAGCGGGCGCGGCCCGCGGCTCTCTGGGCGCCTCTG
DB	2041	CAGGCTGCTCAACTACGAGCGGGCGCGGCCCGCGGCTCTCTGGGCGCCTCTG
QY	2108	CCTGGACGATATCCACAGGCGCTGGCGACCTTCTGTCGTCGTCGGGCGCC
DB	2101	CCTGGACGATATCCACAGGCGCTGGCGACCTTCTGTCGTCGTCGGGCGCC
QY	2168	GCGCCTTGAGCTGTA-----CA
DB	2161	GCGCCTTGAGCTGTA-----CA
QY	2192	GGAACGCTCAGCGAGTCTACGCCAGCATCATCAACCCAGAACACGTACTT
DB	2221	GGAACGCTCAGCGAGTCTACGCCAGCATCATCAACCCAGAACACGTACTT
QY	2252	TCGATATCGCGTGGTCCAGAAAGCCGCCCATGGGCGACGTCCGCAAGGCCCTCA
DB	2281	TCGATATCGCGTGGTCCAGAAAGCCGCCCATGGGCGACGTCCGCAAGGCCCTCA
QY	2312	CGTCTCTACCTTGACAGACCTCAGCGCGTACATGCGACAGTTCGTGGCTCACCT
DB	2341	CGTCTCTACCTTGACAGACCTCAGCGCGTACATGCGACAGTTCGTGGCTCACCT
QY	2372	GACACGCCCTCAGGAGTGCCTGCTGCTCATCGAGCAGAGCTCTCTCCCTGAATG
DB	2401	GACACGCCCTCAGGAGTGCCTGCTGCTCATCGAGCAGAGCTCTCTCCCTGAATG
QY	2432	CAGTGGCTCTTCGAGCTTCTCCTACGCTTTCATGTGCCACACGCGCTGGCAG
DB	2461	CAGTGGCTCTTCGAGCTTCTCCTACGCTTTCATGTGCCACACGCGCTGGCAG
QY	2492	CAAGTCTCAGTCCAGTGCCAGGGGATCCCGAGGGGCTCATCTCTCCACGCT
DB	2521	CAAGTCTCAGTCCAGTGCCAGGGGATCCCGAGGGGCTCATCTCTCTCCACGCT

Db	3661	GAGTGTCCAGCACACCTTGCCTTTCTTCACTTCCCACAGGTGGCGCTCGGCT
Qy	3692	GGGCCAGCTTTTCTCTACACGAGGCCGGCTTCCACTCCCACATAGGAATAG
Db	3721	GGGCCAGCTTTTCTCTACACGAGGCCGGCTTCCACTCCCACATAGGAATAG
Qy	3752	CCGATTTCGCCATTGTTTACCCCTCGGCCCTGCCCTCTCTTTTGCCTTCCACCCCC
Db	3781	CCGATTTCGCCATTGTTTACCCCTCGGCCCTGCCCTCTCTTTTGCCTTCCACCCCC
Qy	3812	AGTGGGAGACCCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGAACAA
Db	3841	AGTGGGAGACCCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGAACAA
Qy	3872	CCCTGTACACAGGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAA
Db	3901	CCCTGTACACAGGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAA
Qy	3932	GAGGTGCTGTGGGAGTAAATACTGTAATATATGAGTTTTTCACTTTTGAAAAA
Db	3961	GAGGTGCTGTGGGAGTAAATACTGTAATATATGAGTTTTTCACTTTTGAAAAA
RESULT 8		
AAH45901		
ID	AAH45901	standard; DNA; 4015 BP.
XX		
AC	AAH45901;	
XX		
DT	06-SEP-2001	(first entry)
XX		
DE		Human hTERT gene.
XX		
KW	Human; hTERT; telomerase; catalytic subunit; mRNA quantitation	
KW	detection; beta-region; diagnosis; cancer; ds.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	exon	1..274
FT		/*tag= a
FT		/number= 1
FT	exon	275..1628
FT		/*tag= b
FT		/number= 2
FT	exon	1629..1824
FT		/*tag= c
FT		/number= 3
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FT		/note= "AAH45908"
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Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY	8	GCAGCGCTCGGCTCTGTGTCGCAAGTGTGGGAAGCCCTGGCCCCCGGACCACCCCCCG
DB	1	GCAGCGCTCGGCTCTGTGTCGCAAGTGTGGGAAGCCCTGGCCCCCGGACCACCCCCCG
QY	68	GCAGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGTGCGCAGCCACCTACCGCGC
DB	61	GCAGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGTGCGCAGCCACCTACCGCGC
QY	128	GCAGCGTGCGCAAGTTTGGTGTGGGCGCTGTGGGCCCCAGGGGTGGCGGCTGTGTC
DB	121	GCAGCGTGCGCAAGTTTGGTGTGGGCGCTGTGGGCCCCAGGGGTGGCGGCTGTGTC
QY	188	GGACCCGGCGGGCTTTCGGCGCGCTGTGTGGCCCACTGCTGGCTGGTGTGCGTGGCCCT
DB	181	GGACCCGGCGGGCTTTCGGCGCGCTGTGTGGCCCACTGCTGGCTGGTGTGCGTGGCCCT
QY	248	AGGGCCGCCCCCCCGCGCGCCCCCTCTTTCGCCCAGGTGTCTCTGCTGAAGGAGC
DB	241	AGGGCCGCCCCCCCGCGCGCCCCCTCTTTCGCCCAGGTGTCTCTGCTGAAGGAGC
QY	308	CCGAGTGTCTGCAGAGACTGTGCAGCGCGCGCGCGAGAACTGTGCTTGGCCTTCG
DB	301	CCGAGTGTCTGCAGAGACTGTGCAGCGCGCGCGCGAGAACTGTGCTTGGCCTTCG
QY	368	GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCCGAGGGCCTTCACACACAGCGTGC
DB	361	GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCCGAGGGCCTTCACACACAGCGTGC
QY	428	CTGTGCCCAACACAGGTGTACACGACCGCATGTGCGGGGGAGCGGGGGCTGCG
DB	421	CTGTGCCCAACACAGGTGTACACGACCGCATGTGCGGGGGAGCGGGGGCTGCG
QY	488	CCGCGTGGCGACGACGTGCTGTGTTTCACTGTGCGACGCTGTGCGCGCTCTTTTG
DB	481	CCGCGTGGCGACGACGTGCTGTGTTTCACTGTGCGACGCTGTGCGCGCTCTTTTG
QY	548	GGTCTCCAGCTGCGCCTACCAAGTGTGTGCGGGCCGCGCTGTACAGCTCGGGCG
DB	541	GGTCTCCAGCTGCGCCTACCAAGTGTGTGCGGGCCGCGCTGTACAGCTCGGGCG
QY	608	TGAGGCGCGGCCCCCGCCACACGCTAGTGTGACCCCGAAGCGTGTGGGATGCG
DB	601	TGAGGCGCGGCCCCCGCCACACGCTAGTGTGACCCCGAAGCGTGTGGGATGCG
QY	668	CTGGAACCATAGCGTTCAGGGAGCCGGGGTCCCGCTGGCGCTGCGACGCCCGCG
DB	661	CTGGAACCATAGCGTTCAGGGAGCCGGGGTCCCGCTGGCGCTGCGACGCCCGCG
QY	728	GAGGCGCGGGGCAGTGCGACGCCAAGTCTGCGGTTGCCCAAGAGGCCACAGGC
DB	721	GAGGCGCGGGGCAGTGCGACGCCAAGTCTGCGGTTGCCCAAGAGGCCACAGGC
QY	788	TGCCCCCTGAGCCGAGCGACCGCGCTGTGGCAGGGGTCTCTGGGCCACCCCGG
DB	781	TGCCCCCTGAGCCGAGCGACCGCGCTGTGGCAGGGGTCTCTGGGCCACCCCGG
QY	848	GGGTGGAACGAGTGAACCGTGTGTTCTGTGTGTGTCACTGTGCAGACCCGCGCG
DB	841	GGGTGGAACGAGTGAACCGTGTGTTCTGTGTGTGTCACTGTGCAGACCCGCGCG
QY	908	CACCTCTTTGGAGGGTGGCTCTCTGGCAGCGGCACCTCCCAACCACTCGTGG
DB	901	CACCTCTTTGGAGGGTGGCTCTCTGGCAGCGGCACCTCCCAACCACTCGTGG
QY	968	GCACCAACGGGGCCCCCATCCACATCGCGGCCACCAAGCTCCTGTGGGACACGC
DB	961	GCACCAACGGGGCCCCCATCCACATCGCGGCCACCAAGCTCCTGTGGGACACGC
QY	1028	CCCGGTGTACGCCGAGACCAAGCATTTCTCTACTCTCTCAGGCGACAGAGGCG
DB	1021	CCCGGTGTACGCCGAGACCAAGCATTTCTCTACTCTCTCAGGCGACAGAGGCG

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standard; cdna; 4015 BP.

(first entry)

reverse transcriptase (TERT) cDNA.

e antigen; alpha(1,3)galactosyltransferase; alpha1.3GT; TERT;
 alpha(1,2)fucosyltransferase; alpha1.2FT; human; enzyme;
 reverse transcriptase; gene; ss.

15.

Location/Qualifiers
 56..3454
 /tag=a
 /product="Human telomerase reverse transcriptase"

1-A2.

XX 26-SEP-2002.
 XX 21-MAR-2002; 2002WO-CA000378.
 XX 21-MAR-2001; 2001US-0277811P.
 XX (GERO-) GERON CORP.
 XX Denning C, Clark AJ, Schiff JM;
 PI WPI; 2002-759895/82.
 DR P-PSDB; AAE29226.
 XX Mammalian cells, useful for producing animal tissues with carb-
 PT antigens that are compatible for transplantation into human pa-
 PT Disclosure; Page 33-34; 71pp; English.
 XX The invention relates to animal tissues with carbohydrate anti-
 CC are compatible for transplantation into human patients. The ma-
 CC cell is inactivated homoygously for expression of alpha(1,3)g-
 CC transferase (alpha1,3GT) gene and comprises a transgene for al-
 CC fucosyltransferase (alpha1,2FT). It is useful for producing an-
 CC with carbohydrate antigens that are compatible for producing an-
 CC human patients. The present sequence is human telomerase rever-
 CC transcriptase (TERT) cDNA used in the invention
 XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
 SQ
 Query Match 98.2%; Score 3933; DB 6; Length 4015;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 3979; Conservative 0; Mismatches 0; Indels 36;
 QY 8 GCAGCGCTGCTCTCTGTCGACAGTGGGAAGCCCTGCGCCCGCCGACACCCCGG
 DB 1 GCAGCGCTGCTCTCTGTCGACAGTGGGAAGCCCTGCGCCCGCCGACACCCCGG
 QY 68 GCGCGCTCCCGCTGCGAGCCGCTGCTCTCTCTGCTGCGCAGCCACTACCGG
 DB 61 GCGCGCTCCCGCTGCGAGCCGCTGCTCTCTCTGCTGCGCAGCCACTACCGG
 QY 128 GCGCGCTGGGCACAGTCTGTCGCGCGCTGCGGCCCGCCAGGGCTGCGGCTGGTGC
 DB 121 GCGCGCTGGGCACAGTCTGTCGCGCGCTGCGGCCCGCCAGGGCTGCGGCTGGTGC
 QY 188 GGNCCCGCGCGCTTTCCGCGCGCTGCTGCGCCAGTCCCTGCTGGTGTGCGTGCCT
 DB 181 GGACCCCGCGGCTTTCCGCGCGCTGCTGCGGCCCGCCAGTCCCTGCTGGTGTGCGTGCCT
 QY 248 ACGGCGCGCCCGCGCGCGCCCTCTCTTCCGCGCGAGGTGCTGCTCAAGGAGC
 DB 241 ACGGCGCGCCCGCGCGCGCCCTCTCTTCCGCGCGAGGTGCTGCTCAAGGAGC
 QY 308 CCGAGTGTCTGACAGAGCTGTGCGAGCGCGCGCGCGAGAAAGCTGCTGGCCCTTCG
 DB 301 CCGAGTGTCTGACAGAGCTGTGCGAGCGCGCGCGAGAAAGCTGCTGGCCCTTCG
 QY 368 GCTGTGTGAGCGGGCCCGCGGGCGCCCGCCCGAGGCTTTACACACAGCGTGC
 DB 361 GCTGTGTGAGCGGGCCCGCGGGCGCCCGCCCGAGGCTTTACACACAGCGTGC
 QY 428 CTTGCCCAACACGCTGACCGAGCGACTGCGGGGAGCGGGGCTGGGGGCTGCT
 DB 421 CTTGCCCAACACGCTGACCGAGCGACTGCGGGGAGCGGGGCTGGGGGCTGCT
 QY 488 CCGCGTGGCGGACGAGCTGCTGCTGCTTACCTGTGCGACGCTGCGGCTCTTTGT
 DB 481 CCGCGTGGCGGACGAGCTGCTGCTGCTTACCTGTGCGACGCTGCGGCTCTTTGT
 QY 548 GCGTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTATACCACTCGGCGC
 DB 541 GCGTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTATACCACTCGGCGC

AGGCCGGCCCGGCCACACGCTAGTGGACCCCGAAGGCGTCTGGATGCGAACGGGC 667
AGGCCGGCCCGGCCACACGCTAGTGGACCCCGAAGGCGTCTGGATGCGAACGGGC 660
GGAAACATAGCGTCAGGGAGGCGGGGTCCTCCCTGGGCTGCGAGCCCGGGTGGAG 727
GGAAACATAGCGTCAGGGAGGCGGGGTCCTCCCTGGGCTGCGAGCCCGGGTGGAG 720
AGCGGGGGGCGAGTGCAGCCGAGTGTGCGCGTTCGCCAAGAGGCGCCAGCGGTGGCG 787
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GCCCTGAGCGCGAGCGGCGCGGTTGGCAGGGGTCTGGGCGCCACCGGGCAGGAC 847
GCCCTGAGCGCGAGCGGCGCGGTTGGCAGGGGTCTGGGCGCCACCGGGCAGGAC 840
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GTGGACCGAGTGACCGTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
ACTCTTTGGAGGGTGGCTCTGTGGACCGGCCACTCCCAATCCGTGGGCGGCCA 967
ACTCTTTGGAGGGTGGCTCTGTGGACCGGCCACTCCCAATCCGTGGGCGGCCA 960
ACACGCGGGCCCGCCATCCACATCGGSCCAGCAGCTCCCTGGGACCGCTGTGTCC 1027
ACACGCGGGCCCGCCATCCACATCGGSCCAGCAGCTCCCTGGGACCGCTGTGTCC 1020
CGGTGTACCGCGAGACCAAGCACTTCCTCTACTCTCAGGGGCAAGGAGCAGCTGCG 1087
CGGTGTACCGCGAGACCAAGCACTTCCTCTACTCTCAGGGGCAAGGAGCAGCTGCG 1080
XCTCTTCTCTACTCAGCTCTCTGAGGCCCGAGCTGAGTGGGCTCGGAGGTCGTGGA 1147
XCTCTTCTCTACTCAGCTCTCTGAGGCCCGAGCTGAGTGGGCTCGGAGGTCGTGGA 1140
CCATCTTCTGGTTCAGGCGCTGGATGCCAGGAGCTCCCGCAGGTTGCGCGCCT 1207
CCATCTTCTGGTTCAGGCGCTGGATGCCAGGAGCTCCCGCAGGTTGCGCGCCT 1200
CCGAGCGCTACTGGCAATGGGCGCCCTGTTTCTGGAGCTGTTGGGAACACACGCA 1267
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GCCCTACGGGGTGTCTCTAAGACGACTCCCGCTCGGAGCTGGCGTCAACCCAGC 1327
GCCCTACGGGGTGTCTCTAAGACGACTCCCGCTCGGAGCTGGCGTCAACCCAGC 1320
CGCGTGTGTGCGCGGAGAACCCAGGGCTCTGTGGCGGCCCGGAGGAGGGA 1387
CGGTGTGTGCGCGGAGAACCCAGGGCTCTGTGGCGGCCCGGAGGAGGGA 1380
CAGACCCCGTGTGCTGTGAGTGTCTCGCCAGCAGCAGCGCCCTGGCAGGTGTA 1447
CAGACCCCGTGTGCTGTGAGTGTCTCGCCAGCAGCAGCGCCCTGGCAGGTGTA 1440
GCTTGTGGGGCTGTGCTGCGCGGCTGGTGGCCCCCAGGCTCTGGGGCTCCAGGCA 1507
GCTTGTGGGGCTGTGCTGCGCGGCTGGTGGCCCCCAGGCTCTGGGGCTCCAGGCA 1500
ACGAACCGCGCTTCTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCCAA 1567
ACGAACCGCGCTTCTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCCAA 1560
TCTCGTGCAGGAGCTACGTGGAGATGAGCTGGGAGCTGGCTTGGCTGGCGAG 1627
TCTCGTGCAGGAGCTACGTGGAGATGAGCTGGGAGCTGGCTTGGCTGGCGAG 1620
GCCCAGGGGTGGCTGTGTTCCGGCCGAGACACCGTCTGCGTGGAGAGTCTTGGC 1687
GCCCAGGGGTGGCTGTGTTCCGGCCGAGACACCGTCTGCGTGGAGAGTCTTGGC 1680

QY 1688 CAAGTTCTGACATGCTGCTGATGATGTGTAGTGTGTAGTGTGTGCTGAGTGTCTCAGGTCTT
Db 1681 CAAGTTCTGCTGCTGCTGCTGATGATGTGTAGTGTGTAGTGTGTGCTGAGTGTCTCAGGTCTT
QY 1748 TGTACCGAGGACCGACGTTTCAAGAAGACAGGCTCTTTTCTACCGGAAGAGTG
Db 1741 TGTACCGAGGACCGACGTTTCAAGAAGACAGGCTCTTTTCTACCGGAAGAGTG
QY 1808 CAAGTTCAAAAGCATTTGGAATCAGACAGACATTTGAAGAGGCTGAGCTGCGGG
Db 1801 CAAGTTGCAAGCATTTGGAATCAGACAGACATTTGAAGAGGCTGAGCTGCGGG
QY 1868 GGAAGCAGAGGTCAGGAGCATCGGGAAGCAGGCCCGCTCTGCTGACGTCCA
Db 1861 GGAAGCAGAGGTCAGGAGCATCGGGAAGCAGGCCCGCTCTGCTGACGTCCA
QY 1928 CTTATCCCCCAAGCCTGACCGGCTGCGGCGATTTGTGAACATGGAATGACTACGTG
Db 1921 CTTATCCCCCAAGCCTGACCGGCTGCGGCGATTTGTGAACATGGAATGACTACGTG
QY 1988 CAGAAGCTTCCGCGAGAAAGAGGCGCGAGCGTCTCACCTCGAGGCTGAAGG
Db 1981 CAGAAGCTTCCGCGAGAAAGAGGCGCGAGCGTCTCACCTCGAGGCTGAAGG
QY 2048 CAGGTGCTCAACTAGAGCGGCGCGGCGCCCGCTCTCTGGGCGCTCTG
Db 2041 CAGGTGCTCAACTAGAGCGGCGCGGCGCCCGCTCTCTGGGCGCTCTG
QY 2108 CTTGGACGATATCCACAGGCGCTGCGGCGACCTTCGTGCTGCTGCTGCGGCGCC
Db 2101 CTTGGACGATATCCACAGGCGCTGCGGCGACCTTCGTGCTGCTGCGGCGCC
QY 2168 GCCGCTGAGCTGTA-----CA-
Db 2161 GCCGCTGAGCTGTA-----CA-
QY 2192 GGAAGGCTCAGGAGGTCATCGCAGCATCATCAAAACCCAGAAACACGCTACT
Db 2221 GGAAGGCTCAGGAGGTCATCGCAGCATCATCAAAACCCAGAAACACGCTACT
QY 2252 TCGGTATCGGTGCTCCAGAGCGCCCGCTGAGGCGAGCTCGGAGGCGCTTCAJ
Db 2281 TCGGTATCGGTGCTCCAGAGCGCCCGCTGAGGCGAGCTCGGAGGCGCTTCAJ
QY 2312 CGTCTCTACTTTCAGACAGCTCCAGCGCTACATGCGACAGTTCGTGGCTCACCT
Db 2341 CGTCTCTACTTTCAGACAGCTCCAGCGCTACATGCGACAGTTCGTGGCTCACCT
QY 2372 GACCAGCGCTGAGGAGTGGCGTCTCATCGAGCAGAGCTCTCTCTGAAATG
Db 2401 GACCAGCGCTGAGGAGTGGCGTCTCATCGAGCAGAGCTCTCTCTGAAATG
QY 2432 CAGTGGCTCTTCGAGCTCTTCTTACGCTTCTATGCTGCGACACGCGCTGCGGCAI
Db 2461 CAGTGGCTCTTCGAGCTCTTCTTACGCTTCTATGCTGCGACACGCGCTGCGGCAI
QY 2492 CAAAGTCTACGTCAGTGCAGGGATCCCGAGGCGCTCCATCTCTCCACGCT
Db 2521 CAAAGTCTACGTCAGTGCAGGGATCCCGAGGCGCTCCATCTCTCCACGCT
QY 2552 CAGCTGTGCTACGCGGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGGA
Db 2581 CAGCTGTGCTACGCGGACATGGAGAACAGCTGTTTGGGGGATTCGGCGGGA
QY 2612 GCTCTGCTGTTTGGTGGATGATTTCTTCTGTTGCTGACACTCACCTCACCGCG
Db 2641 GCTCTGCTGTTTGGTGGATGATTTCTTCTGTTGCTGACACTCACCTCACCGCG
QY 2672 CTTCTCAGGACCTTGGTCCGAGGTCCTCTGAGTATGCTGCTGCGTGGTGAATT
Db 2701 CTTCTCAGGACCTTGGTCCGAGGTCCTCTGAGTATGCTGCTGCGTGGTGAATT
QY 2732 GACAGTGTGAATTCCTCTGTAGAAGACGAGGCCCTGGGTGGCACGCGCTTTGT

Db	3841	AGSTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCA		
Qy	3872	CCCTGTACAGGGGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCA		
Db	3901	CCCTGTACAGGGGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAA		
Qy	3932	GAGTGCTGTGGGAGTAAATACTGTAATATATGAGTTTTTCAGTTTTGAAAA		
Db	3961	GAGTGCTGTGGGAGTAAATACTGTAATATATGAGTTTTTCAGTTTTGAAAA		
RESULT 10				
ABA97534				
ID	ABA97534	standard; DNA; 4015 BP.		
XX	AC	ABA97534;		
XX	DT	05-APR-2002 (first entry)		
XX	DE	Cancer cell discrimination method related human DNA.		
XX	KW	Human; telomerase; enzyme; cancer cell discrimination; gene;		
XX	KW	reverse transcriptase; ds.		
XX	OS	Homo sapiens.		
XX	PN	JP2001309791-A.		
XX	PD	06-NOV-2001.		
XX	PF	02-MAY-2000; 2000JP-00138250.		
XX	PR	02-MAY-2000; 2000JP-00138250.		
XX	PA	(KANE/) KANEUCHI H.		
XX	PA	(KAMI/) KAMIMORI M.		
XX	DR	WPI; 2002-134853/18.		
XX	PT	Discrimination of a cancer cell in a sample tissue, comprises		
XX	PT	the expression level of a reverse transcriptase component of t		
XX	PT	using a hybridization assay.		
XX	PS	Claim 2; Page 9-10; 16pp; Japanese.		
XX	CC	The present invention relates to a method for the discriminati		
XX	CC	cancer cell in a sample tissue, which involves determining the		
XX	CC	level of a reverse transcriptase component of telomerase in a		
XX	CC	constituting the sample tissue by an in situ hybridization of		
XX	CC	the enzyme, and judging a cell showing a higher expression lev		
XX	CC	that of the reverse transcriptase component of telomerase in a		
XX	CC	cell to be a cancer cell. The present sequence is a human DNA		
XX	CC	exemplification of the invention		
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;			
Query Match 98.2%; Score 3933; DB 6; Length 4015;				
Best Local Similarity 99.1%; Pred. No. 0;				
Matches 3979; Conservative 0; Mismatches 0; Indels 36;				
Qy	8	GCAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGGCACCCCGCG		
Db	1	GCAGCGCTGGTCTGCTGCTGGCACGTGGAGCCCTGGCCCCGGGCACCCCGCG		
Qy	68	GCGCGCTCCCGCTCCGAGCGGTGCGTCCCTGTGCGCAGCCACTACCGCGP		
Db	61	GCGCGCTCCCGCTCCGAGCGGTGCGTCCCTGTGCGCAGCCACTACCGCGA		
Qy	128	GCGCGTGGCCAGTTCGTGCGGCGCTGGGGCCCCCAGGGCTGGGGCTGGTGA		
Db	121	GCGCGTGGCCAGTTCGTGCGGCGCTGGGGCCCCCAGGGCTGGGGCTGGTGA		
Qy	188	GGACCCGGCGGCTTTCCCGCGGCGCTGGTGGCCGACAGTGGCTGGTGGCGCTG		

ACCAGCCCGCTGAGGAGTGCCTGCTCATCGAGCAGAGCTCCTCCCTGAAATGAGGCCAG 2431
 |||||
 ACCAGCCCGCTGAGGAGTGCCTGCTCATCGAGCAGAGCTCCTCCCTGAAATGAGGCCAG 2460
 |||||
 AGTGGCCCTCTTCGAGCGTCTTCCTACGCTTCATGTGCGCAACACGCGCTGCGCATCAGGGG 2491
 |||||
 AGTGGCCCTCTTCGAGCGTCTTCCTACGCTTCATGTGCGCAACACGCGCTGCGCATCAGGGG 2520
 |||||
 AAGTCCCTACGCTCCAGTGCAGAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG 2551
 |||||
 AAGTCCCTACGCTCCAGTGCAGAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG 2580
 |||||
 AGCTGTGCTACGCGCGCATGGAGAACAAAGCTGTTTGGGGGATTCGGCGGGACGGGCT 2611
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 AGCTGTGCTACGCGCGCATGGAGAACAAAGCTGTTTGGGGGATTCGGCGGGACGGGCT 2640
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 |||||
 TCTCTCGGTTTGGTGGATGATTTCTTGTGGTGAACACTCAGCTCAGCCACCGGAAAC 2700
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 TTCTCAGGACCTCTGGTCCGAGGTGCTCCCTGAGTATGCTGCGTGGTGGTGGTGGTGGT 2731
 |||||
 TTCTCAGGACCTCTGGTCCGAGGTGCTCCCTGAGTATGCTGCGTGGTGGTGGTGGTGGT 2760
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 ACAGTGTGAATCTTCCCTGTAGAGACGAGGCGCTTGGTGGTGGTGGTGGTGGTGGTGGT 2791
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 ACAGTGTGAATCTTCCCTGTAGAGACGAGGCGCTTGGTGGTGGTGGTGGTGGTGGTGGT 2820
 |||||
 TCGGCCACGGCTATTCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2851
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 TCGGCCACGGCTATTCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2880
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 TAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2911
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 TAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940
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 |||||
 TAGAGCTGTTCTGATTTGCAAGGTGAACAGCGCTCCAGCGGTGTCACCAACATCTA 3031
 |||||
 TAGAGCTGTTCTGATTTGCAAGGTGAACAGCGCTCCAGCGGTGTCACCAACATCTA 3060
 |||||
 TAGATCCTCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGCTGAGCTCCCATTTCA 3091
 |||||
 TAGATCCTCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGCTGAGCTCCCATTTCA 3120
 |||||
 TAGCAAGTTTGGAGAACCCCAATTTTCTGCGGCTCATCTGACACGCGCTCCCT 3151
 |||||
 TAGCAAGTTTGGAGAACCCCAATTTTCTGCGGCTCATCTGACACGCGCTCCCT 3180
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 TGTACTCTCATCTGAAAGCAGAGGATGCTGCTGGGGCCAGAGGCGCGC 3211
 |||||
 TGTACTCTCATCTGAAAGCAGAGGATGCTGCTGGGGCCAGAGGCGCGC 3240
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 TGGCTCTGCTGCTGAGGCGGTGAGTGGCTGTGCGCACCAAGCATTTCTGCTCAAGCT 3300
 |||||
 TCGGACACGCTGTACCTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCAGACGCA 3331
 |||||
 TCGGACACGCTGTACCTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCAGACGCA 3360
 |||||
 TGAGTCCGAAGCTCCCGGGGACGCGTCACTGCTGGAGGCGCGCAGCAACCGGC 3391
 |||||
 TGAGTCCGAAGCTCCCGGGGACGCGTCACTGCTGGAGGCGCGCAGCAACCGGC 3420
 |||||
 TGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCCCGCCACAGCCAGGCCGA 3451
 |||||
 TGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCCCGCCACAGCCAGGCCGA 3480

QY 3452 GAGCAGACACAGCAGCCCTGTCTACGCCGGGCTCTACGTCCAGGAGGGAGG 3481
 |||||
 Db 3481 GAGCAGACACAGCAGCCCTGTCTACGCCGGGCTCTACGTCCAGGAGGGAGG 3512
 |||||
 QY 3512 CACACCCAGGCCCCCAGCCGCTGGGAGTCTGAGGCTCTGAGTGGTGGTGGGCGG 3541
 |||||
 Db 3541 CACACCCAGGCCCCCAGCCGCTGGGAGTCTGAGGCTCTGAGTGGTGGTGGGCGG 3572
 |||||
 QY 3572 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTCTGAGGAGTGTCCAGCC 3601
 |||||
 Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTCTGAGGAGTGTCCAGCC 3632
 |||||
 QY 3632 GAGTGTCCAGCACACCTGCGCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTC 3661
 |||||
 Db 3661 GAGTGTCCAGCACACCTGCGCTCTTCACTTCCCCACAGGCTGGCGCTCGGCTC 3692
 |||||
 QY 3692 GGGCCAGCTTTTCTCTACAGGAGCCCGGCTTCCACTCCCCACATAGGAATAG 3721
 |||||
 Db 3721 GGGCCAGCTTTTCTCTACAGGAGCCCGGCTTCCACTCCCCACATAGGAATAG 3752
 |||||
 QY 3752 CCAGATTCCGCTATTTTCACTCCCTCGGCTCGGCTCTTGGCTTCCAGCCCC 3781
 |||||
 Db 3781 CCAGATTCCGCTATTTTCACTCCCTCGGCTCGGCTCTTGGCTTCCAGCCCC 3812
 |||||
 QY 3812 AGGTGGAGACCCCTGAGAGGACCTCGGAGCTCTGGGAAATTTGGAGTGACCA 3841
 |||||
 Db 3841 AGGTGGAGACCCCTGAGAGGACCTCGGAGCTCTGGGAAATTTGGAGTGACCA 3872
 |||||
 QY 3872 CCTGTACACAGCGAGGACCCCTGACCTGGGCTCGGCTCTTGGGCTCAAA 3901
 |||||
 Db 3901 CCTGTACACAGCGAGGACCCCTGACCTGGGCTCGGCTCTTGGGCTCAAA 3932
 |||||
 QY 3932 GAGGTGCTGGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTGAAAAA 3961
 |||||
 Db 3961 GAGGTGCTGGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTGAAAAA

RESULT 11
 ACC58039
 ID ACC58039 standard; cDNA; 4015 BP.
 XX AC ACC58039;
 XX XX
 DT 11-AUG-2003 (first entry)
 XX Human telomerase reverse transcriptase cDNA.
 DE Telomerase reverse transcriptase; TERT; enzyme; RNA interferent
 XX short interfering RNA; siRNA; cancer; tumour; cytosolic; cont
 KW immunosuppressive; antiinfertility; fungicide; antiparasitic;
 KW antiinflammatory; human; gene therapy; gene; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 56..3454
 CDS /*tag= a
 FT /product= "TERT"
 FT
 XX
 PN W02003035667-A2.
 XX
 XX 01-MAY-2003.
 XX
 PF 16-OCT-2002; 2002WO-US033065.
 XX
 PR 22-OCT-2001; 2001US-0345326P.
 PR 20-FEB-2002; 2002US-0359196P.
 PR 22-MAY-2002; 2002US-0383195P.
 XX
 PA (UYRP) UNIV ROCHESTER.
 XX Rowley PT;
 PI
 XX

103336/38.
142384.

le-stranded short interfering RNA having sense and antisense
ids which are complementary to each other and to target nucleic
telomerase RNA or mRNA encoding telomerase reverse
ase.

: Fig 3A-B; 37pp; English.

: sequence is that of human telomerase reverse transcriptase 1. The invention relates to the discovery that double-stranded RNAs, such as short interfering RNAs (siRNA), which target RNA or TERT mRNA are capable of inhibiting telomerase inhibition of telomerase in cancer cells leads to telomere end-to-end chromosomal fusion, and apoptosis. Interference of activity can also be used for treatment of infertility, for on or sterilisation, for immunosuppression, for treatment of virus and fungal infections, and in anti-inflammatory therapies. Use is active in a limited number of cell types, e.g. tumour cell lines, certain stem cells of the haematopoietic system, T cells, sun-damaged skin, and proliferative cervix, most normal cells not affected by telomerase RNA interference therapy

)15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Similarity 98.2%; Score 3933; DB 7; Length 4015;
99.1%; Pred. No. 0;

Conservative	0	Mismatches	0	Indels	36	Gaps	1
Conservative	0 <td>Mismatches</td> <td>0 <td>Indels</td> <td>36</td> <td>Gaps</td> <td>1</td> </td>	Mismatches	0 <td>Indels</td> <td>36</td> <td>Gaps</td> <td>1</td>	Indels	36	Gaps	1

AGCGCTGCGTCTTGCTGCGACGTGGGAAGCCCTGGCCCCGGCCACCCCCGGATGCC 67

AGCGCTGCGTCCTGTGCTGCCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGGATGCC 60

5'-GGCTCCCGCTGCCGAGCCGTGGCTCCCTGCTGGCAGCACTACCGGAGGTGCT-3'

5'-GGCTCCCCGCTGCCGAGCCGTGGCTCCCTGCTGGCAGCCACTACCGGAGGTGCT-3'

CGCTGGCCACGTTCTGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGACAGCGCG 18

'CGCTGGCCACGTTCTGTGCGGGCCCTGGGGCCCCAGGGCTGGCGGCTGGTGACAGCGCG 180

!ACCGGGGGCTTTCGGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGGGACGC 247

!ACCGGGCGGCTTCCGGCGGCTGGTGGCCAGTGCCCTGGTGTGGCTGCCCTGGGACGC 240

'GGCGGCCCCCGCGGCCCTCCTTCGCCAGGTGTCTGCCCTGAAGAGCTGGTGGC 30'

'GGCGGCCCCCGCGGCCCTCCTTCGCGAGGTGCTCCCTGAAGAGCTGGTGGC 300

'GAGTGCTGCAGAGGCTGTGCGAGCGCGCGGAAGAACGTGCTGGCCTTCGGCTTCGC 367

GAGTGTGCAGAGGCTGTGGAGCGCGCGAAGACGTGTGGCCTTGGCTTCG 360

TGCTGGACGGGGCCCGGGGGCCCCCGAGGCCCTCACCAACGCGTGCGCAGCTA 427

TGCTGGACGGGGCCCGGGGGCCCCCGAGGCCCTCACACCAGCGTGCGCAGCTA 420

TGCCCAACACGGTGACCGACCGACTCGCGGGGAGCGGGGCGTGGGGCGTCTGCTGCG 487

TGCCCAACACGGTGACCGACCGACTGCGGGGAGCGGGGCTGCTGCTGCG 480

'GCGTGGGCGACGACGTGCTGGTTCACTGCTGGCACGCTGGCGCTCTTTGTGCTGGT 547

'GGGTGGGGCGACGACGTGCTGGTTCACTGCTGGCACGCTGCGGCTCTTTGTGCTGGT 540

CTCCAGCTGCGCCCTACCAAGGTGTGGGGCGCGCTGTACCAAGCTCGGCGTCCAC 607

CTCCAGCTGGCCCTACAGGTGTGGGGCCGCGTGTACCACTCGGCGTGCCAC 600

AGGCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGCCGAACGGGC 667

AGGCCGGCCCCCGCCACACGCTAGTGGACCCCGAGGGCGTCTGGGATGCCAACGGGC 660

2821	Db	GCCGGCCACAGGCGCTATTTCCTCTGGTGGGCGCTGCTGCTGATACC CGGACCG
2852	QY	GCAGAGGACTACTCTCAGCTATGCCCAGGACCTCCCATAGAGCCAGTCTCACT
2881	Db	GCAGAGGAGTACTCTCAGCTATGCCCGGACCTCCCATCAGAGCCAGTCTCACT
2912	QY	CGGCTTCAAGGCTGGAGGAACTGCGTCGCAAACTCTTTGGGGCTCTTGCGGC
2941	Db	CGGCTTCAAGGCTGGAGGAACTGCGTCGCAAACTCTTTGGGGCTCTTGCGGC
2972	QY	TCACAGGCTGTTCCTGGATTTCAGAGTGAA CAGGCTCCAGACGGTGTGCACCA
3001	Db	TCACAGGCTGTTCCTGGATTTCAGAGTGAA CAGGCTCCAGACGGTGTGCACCA
3032	QY	CAAGATCTCTGCTGTCAGGCGTACAGTTTCA CGCATGTGTGCTGCAGCTCC
3061	Db	CAAGATCTCTGCTGTCAGGCGTACAGTTTCA CGCATGTGTGCTGCAGCTCC
3092	QY	TCAGCAAGTTTGGAGAACCCCAATTTTTCCT GCGGTCATCTCTGACACGG
3121	Db	TCAGCAAGTTTGGAGAACCCCAATTTTTCCT GCGGTCATCTCTGACACGG
3152	QY	CTGCTACTCCATCTCTGAAGCCAAAGAACG CAGGATGTGCTGGGGGCGCAAGG
3181	Db	CTGCTACTCCATCTCTGAAGCCAAAGAACG CAGGATGTGCTGGGGGCGCAAGG
3212	QY	CGGCCCTCTGCGCTCCAGGCGGTGCAGTGGCT GTGCGCA CCAAGCATTCCTGCG
3241	Db	CGGCCCTCTGCGCTCCAGGCGGTGCAGTGGCT GTGCGCA CCAAGCATTCCTGCG
3272	QY	GACTCGACACCGTGTCACTTACGTGTCACAT CTTGGGTCATCTCAGGACAGGCC
3301	Db	GACTCGACACCGTGTCACTTACGTGTCACAT CTTGGGTCATCTCAGGACAGGCC
3332	QY	GCTGAGTCGGAAGCTCCCGGGGACGACGCTG CACTGCTCGAGGCCCGCAGGCCA
3361	Db	GCTGAGTCGGAAGCTCCCGGGGACGACGCTG CACTGCTCGAGGCCCGCAGGCCA
3392	QY	ACTGCCCTCAGACTTCAAGACCATCTCTGAC ATGATGCGCACCCGCGCCACAGCC
3421	Db	ACTGCCCTCAGACTTCAAGACCATCTCTGAC ATGATGCGCACCCGCGCCACAGCC
3452	QY	GAGCAGACACAGCAGCCCTGTACGCGCGGCT CTAAGTCCCGAGGAGGAGG
3481	Db	GAGCAGACACAGCAGCCCTGTGTACGCGCGG CTCTACGTCCCAGGAGGAGGAGG
3512	QY	CACACCCAGCCCGCACCGCTGGAGTCTCAGG CCTCAGTGAGTGTGTGCGCG
3541	Db	CACACCCAGCCCGCACCGCTGGAGTCTCAGG CCTCAGTGAGTGTGTGCGCG
3572	QY	CATGTCCGCTGAAGGCTGAGTGTCCGGCTGAG GCGCTGAGCGAGTGTCCAGCC
3601	Db	CATGTCCGCTGAAGGCTGAGTGTCCGGCTGAG GCGCTGAGCGAGTGTCCAGCC
3632	QY	GAGTGTCCAGCACACTGCGCTCTCACTTCCC CACAGGCTGCGGCTCGGCTC
3661	Db	GAGTGTCCAGCACACTGCGCTCTCACTTCCC CACAGGCTGCGGCTCGGCTC
3692	QY	GGGCCAGCTTTTCTCACAGGAGCCCGCTTCC ACTCCCACATAGGAATAG
3721	Db	GGGCCAGCTTTTCTCACAGGAGCCCGCTTCC ACTCCCACATAGGAATAG
3752	QY	CCAGATTGCGCATTTGTTCA CCGCTCGCCTTGCCCTCTTTGCGCTTCCACCCCG
3781	Db	CCAGATTGCGCATTTGTTCA CCGCTCGCCTTGCCCTCTTTGCGCTTCCACCCCG
3812	QY	AGGTGGAGACCTTGAGAAAGGACCTGGAGCT CTGGGAATTTGGAGTGACCAAT
3841	Db	AGGTGGAGACCTTGAGAAAGGACCTGGAGCT CTGGGAATTTGGAGTGACCAAT
3872	QY	CCCTGTACACAGCGCAGGACCTTGCACTTGGA ATGGGGGTCCCTGTGCGGTCAAAAT

CGTGTACACAGGCGAGGACCTGCACCTGGATGGGGTCCCTGTGGGTCAATTTGGGG 3960
AGGTGCTGTGGAGTAAATCTGAATATATGAGTTTTCAGTTTGTGAAAAA 3986
AGGTGCTGTGGAGTAAATCTGAATATATGAGTTTTCAGTTTGTGAAAAA 4015

standard; cDNA; 4015 BP.

3 (first entry)

merase reverse transcriptase cDNA.

reverse transcriptase; TERT: enzyme; RNA interference;
referring RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
ressive; antiinfertility; fungicide; antiparasitic;
matory; human; gene therapy; gene; ss.

ns.

Location/Qualifiers

56..3454

/*tag= a

/product= "TERT"

85-A2.

3.

2; 2002WO-US033146.

1; 2001US-0345326P.

2; 2002US-0359196P.

2; 2002US-0383195P.

IV ROCHESTER.

103289/38.

342063.

ic acid encoding or comprising interfering RNAs which target
RNA, useful for inhibiting telomerase activity for treating
fertility and disorders of the immune system.

; Fig 3; 52pp; English.

; sequence is that of human telomerase reverse transcriptase
1. The invention relates to the discovery that double-stranded
RNAs, such as short interfering RNAs (siRNA), which target
RNA or TERT mRNA are capable of inhibiting telomerase
inhibition of telomerase in cancer cells leads to telomere
end-to-end chromosomal fusion, and apoptosis. Interference of
activity can also be used for treatment of infertility, for
on or sterilisation, for immunosuppression, for treatment of
site and fungal infections, and in antiinflammatory therapies.
use is active in a limited number of cell types, e.g. tumour
line cells, certain stem cells of the haematopoietic system, T
i, sun-damaged skin, and proliferative cervix, most normal
not affected by telomerase RNA interference therapy

115 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

ilarity 98.2%; Score 3933; DB 7; Length 4015;

Conservative 0; Mismatches 0; Indels 36; Gaps 1;

'AGCGTGGCTCCTGTGCGCACGTGGGAGCCCTGGCCCCCGCCACCCCGCGATGCC 67

Db 1 GCAGCGCTCGCTCTGCTGCGCACGTGGAAGCCCTGGCCCCCGGCACACCCG
QY 68 GGGCGCTCCCGCTGCGGAGCGGTGCGTCCCTGCTGCGGACCGACTACCGC
Db 61 GGGCGCTCCCGCTGCGGAGCGGTGCGTCCCTGCTGCGGACCGACTACCGC
QY 128 GCGCGTGGCCACGTTCTGTCGCGCGCTGCGGCGCCCGAGGCGTGGCGGTG
Db 121 GCGCGTGGCCACGTTCTGTCGCGCGCTGCGGCGCCCGAGGCGTGGCGGTG
QY 188 GAGCCCGCGGCTTTCGCGCGCTGCGTGGCGCCCGAGTGCCTGCTGCGTGC
Db 181 GAGCCCGCGGCTTTCGCGCGCTGCGTGGCGCCCGAGTGCCTGCTGCGTGC
QY 248 ACGGCGCGCCCGCGCGCCCTCTCTCCGCGCAGGTGCTCTGCTGAAAGGAG
Db 241 ACGGCGCGCCCGCGCGCCCTCTCTCCGCGCAGGTGCTCTGCTGAAAGGAG
QY 308 CCGAGTGTGCGAGGCTGTGCGAGCGCGCGCGGCGGAAACGTCGTGGCTTC
Db 301 CCGAGTGTGCGAGGCTGTGCGAGCGCGCGCGCGGCGGAAACGTCGTGGCTTC
QY 368 GCTGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 361 GCTGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 428 CCTGCCAACAACGCTGACCGAGCGACTGCGGGGAGCGGGCGCTGGGGCTGC
Db 421 CCTGCCAACAACGCTGACCGAGCGACTGCGGGGAGCGGGCGCTGGGGCTGC
QY 488 CCGCGTGGCGGACGACGCTGCTGCTTCACTCTGCGCAGCGCTGCGCTCTTTG
Db 481 CCGCGTGGCGGACGACGCTGCTGCTTCACTCTGCGCAGCGCTGCGCGCTCTTTG
QY 548 GGTCTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCGCGCTGTACAGCTCGGCG
Db 541 GGTCTCCAGCTGCGCTTACAGAGTGTGCGGCGCGCGCGCTGTACAGCTCGGCG
QY 608 TCAGGCG
Db 601 TCAGGCG
QY 668 CTGGAACCATAGCGTCAAGGAGCGCGGCGTCCCGCTGCGGCTGCGAGCCCGG
Db 661 CTGGAACCATAGCGTCAAGGAGCGCGGCGTCCCGCTGCGGCTGCGAGCCCGG
QY 728 GAGCGCGGCGGAGTGCAGCGAAGTCTGCGGTTGCCAAGAGGCGCGAGGC
Db 721 GAGCGCGGCGGAGTGCAGCGAAGTCTGCGGTTGCCAAGAGGCGCGAGGC
QY 788 TGCCCTCTGAGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Db 781 TGCCCTCTGAGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY 848 GCGTGGACCGAGTACCGTGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG
Db 841 GCGTGGACCGAGTACCGTGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG
QY 908 CACTCTTTGGAGGGTGGCTCTCTGCGCAGCGGCGCACTCCCGACCCATCGTGG
Db 901 CACTCTTTGGAGGGTGGCTCTCTGCGCAGCGGCGCACTCCCGACCCATCGTGG
QY 968 GCACACGCGGCG
Db 961 GCACACGCGGCG
QY 1028 CCGGTGTGTACGGCGAGACCAAGCACTTCTCTACTCTCAGGCGCAAGGAGC
Db 1021 CCGGTGTGTACGGCGAGACCAAGCACTTCTCTACTCTCAGGCGCAAGGAGC
QY 1088 GCGCTCTCTCTACTCAGCTCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCG

CCCTCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTCGTGA 1140
ACATCTTTCTGGTTCCAGGCTTGTGATGCGAGGACTCTCCCGGAGGTTGCCCGCGCT 1207
ACATCTTTCTGGTTCCAGGCTTGTGATGCGAGGACTCTCCCGGAGGTTGCCCGCGCT 1200
CCAGCGCTACTGGCAAAATGGCGCCCTCTTTCTGGAGCTGTCTGGGAACACACGGCA 1267
CCAGCGCTACTGGCAAAATGGCGCCCTCTTTCTGGAGCTGTCTGGGAACACACGGCA 1260
TGCCCTTACGGGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACTCCGAGC 1327
TGCCCTTACGGGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACTCCGAGC 1320
CCGGTGTCTGTGCGCGGAGAGGCCAGGCTCTGTGCGCGCCCGCGAGGAGGAGGA 1387
CCGGTGTCTGTGCGCGGAGAGGCCAGGCTCTGTGCGCGCCCGCGAGGAGGAGGA 1380
ACAGACCCCGCTCGCTGTGTCAGCTGCTCGCCAGCACAGACAGCCCTCGCAGGTGTA 1447
ACAGACCCCGCTCGCTGTGTCAGCTGCTCGCCAGCACAGACAGCCCTCGCAGGTGTA 1440
CGCTTGTGCGGGCTGCTCGCGCGCTGCTGCGCGCCCGCGAGGCTCTCGAGGCTCCAGGCA 1507
CGCTTGTGCGGGCTGCTCGCGCGCTGCTGCGCGCCCGCGAGGCTCTCGAGGCTCCAGGCA 1500
ACGAGCGCGCTTCTCAGGAACACCAAGAGTTCACTCTCCCTGGGGAGCATGCCAA 1567
ACGAGCGCGCTTCTCAGGAACACCAAGAGTTCACTCTCCCTGGGGAGCATGCCAA 1560
CTCTCGTGCAGGAGCTGAGCTGGAAGATGAGCGTGGGACTGCGCTTGGCTGGCGAG 1627
CTCTCGTGCAGGAGCTGAGCTGGAAGATGAGCGTGGGACTGCGCTTGGCTGGCGAG 1620
AGCCAGGGGTGGCTGTGTTCCGCGCGCAGACACCGTCTGCGTGAGGAGATCTCTGGC 1687
AGCCAGGGGTGGCTGTGTTCCGCGCGCAGACACCGTCTGCGTGAGGAGATCTCTGGC 1680
AGTTCTCGTGCAGTGTGATGATGTGATGCTGTGCTGAGCTGCTCAGGTCTTCTTTTA 1747
AGTTCTCGTGCAGTGTGATGATGTGATGCTGTGCTGAGCTGCTCAGGTCTTCTTTTA 1740
CTCAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1807
CTCAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG 1800
AGTTGCAAAAGCATTGAATCAGACAGCACTTGAAGGGTGTGAGTGTGCGGAGCTGTG 1867
AGTTGCAAAAGCATTGAATCAGACAGCACTTGAAGGGTGTGAGTGTGCGGAGCTGTG 1860
AAGCAGAGGTCAAGGAGCATTCGGGAAGCCAGCCCGCTGTGAGCTCCAGACTCCG 1927
AAGCAGAGGTCAAGGAGCATTCGGGAAGCCAGCCCGCTGTGAGCTCCAGACTCCG 1920
TTTATCCCCAAGCCTGACGGGCTGCGCGCGAATTTGTAACATGGACTACGTCGTGGGAGC 1987
TTTATCCCCAAGCCTGACGGGCTGCGCGCGAATTTGTAACATGGACTACGTCGTGGGAGC 1980
AGAACGTTCCGAGAGAAAGAGGCCGAGGCTCTACCTCGAGGGTGAAGGCACTGTT 2047
AGAACGTTCCGAGAGAAAGAGGCCGAGGCTCTACCTCGAGGGTGAAGGCACTGTT 2040
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AGCGTGTCTCAACTACGAGCGGGCGCGCCCGCTCTGGCGCTCTGTGCTGGG 2100
CTGAGCATATCCACAGGGCTGCGCGACCTTCTGTGCTGCTGTGCGGGCCCGAGGACC 2167
CTGAGCATATCCACAGGGCTGCGCGACCTTCTGTGCTGCTGTGCGGGCCCGAGGACC 2160
CCGCTGAGCTGTA-----CATCCCCCA 2191
CCGCTGAGCTGTA-----CATCCCCCA 2220

2192 GGACAGGCTCAGGAGGTGATCGCCAGCATCATCAAAACCCAGAACAGTACT
2221 GGACAGGCTCAGGAGGTGATCGCCAGCATCATCAAAACCCAGAACAGTACT
2252 TCGGTATGCGGTGTCAGAAAGCGCGCCATGGGACAGTCCGCAAGGCTTCA
2281 TCGGTATGCGGTGTCAGAAAGCGCGCCATGGGACAGTCCGCAAGGCTTCA
2312 CGTCTTACCTTGAACAGACCTCCAGCCGTACATGCGACAGTTCTGTGCTCACC
2341 CGTCTTACCTTGAACAGACCTCCAGCCGTACATGCGACAGTTCTGTGCTCACC
2372 GACAGCCCGCTGAGGATGCGCTGCTCATGCGAGGAGCTCTCTCCGTGAATG
2401 GACAGCCCGCTGAGGATGCGCTGCTCATGCGAGGAGCTCTCTCCGTGAATG
2432 CAGTGGGCTCTTGCAGCTCTTCTTACGCTTTCATGTGCCACACAGCCCTGGGCA
2461 CAGTGGGCTCTTGCAGCTCTTCTTACGCTTTCATGTGCCACACAGCCCTGGGCA
2492 CAAGTCTTACGTCAGTGCAGGGGATCCCGAGGGCTCCATCTCTTCCACGC
2521 CAAGTCTTACGTCAGTGCAGGGGATCCCGAGGGCTCCATCTCTTCCACGC
2552 CAGCCTGTGTAGCGGACATGAGACAGCTGTTTGGGGGATTCGGGGGG
2581 CAGCCTGTGTAGCGGACATGAGAAAGCTGTTTGGGGGATTCGGGGGG
2612 GCTCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACG
2641 GCTCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACG
2672 CTCTCTCAGACCCCTGTGCGAGGTGCTCCTGAGTATGGCTGTGCTGTGAACT
2701 CTCTCTCAGACCCCTGTGCGAGGTGCTCCTGAGTATGGCTGTGCTGTGAACT
2732 GACAGTGTCAACTTCCCTCTAGAAAGAGGCGCTGGGTGGGACGCTTTTG
2761 GACAGTGTCAACTTCCCTCTAGAAAGAGGCGCTGGGTGGGACGCTTTTG
2792 GCGGGCCACAGGCTATTTCCCTCTGGTGGCGCTGCTGCTGGATACCCGAGCCC
2821 GCGGGCCACAGGCTATTTCCCTCTGGTGGCGCTGCTGCTGGATACCCGAGCCC
2852 GCAGAGGACTACTCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCAGCT
2881 GCAGAGGACTACTCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCAGCT
2912 CGGCTTCAAGGCTGGGAGGAACATGCGTCCGAAACTCTTTGGGGTCTTGGCGG
2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCCGAAACTCTTTGGGGTCTTGGCGG
2972 TCACAGCCTGTTTCTGGAATTCAGGTGAACAGCCTCCAGACGGTGTGACCA
3001 TCACAGCCTGTTTCTGGAATTCAGGTGAACAGCCTCCAGACGGTGTGACCA
3032 CAAGATCCTCTGTGCGAGGCTACAGGTTTCAAGCATGTGTGCTGCGAGTCC
3061 CAAGATCCTCTGTGCGAGGCTACAGGTTTCAAGCATGTGTGCTGCGAGTCC
3092 TCAGCAAGTTTGAAGAAACCCACATTTTCTCGCGCTCATCTCTGACACGG
3121 TCAGCAAGTTTGAAGAAACCCACATTTTCTCGCGCTCATCTCTGACACGG
3152 CTGCTACTCATCTGAAAGCCAAAGAACGAGGGATGTGCTGGGGGCCAAGG
3181 CTGCTACTCATCTGAAAGCCAAAGAACGAGGGATGTGCTGGGGGCCAAGG
3212 CGGCTCTGCTCTCGAGGCGCTGAGTGGCTGTGCGCACCAAGCATTTCTGCT
3241 CGGCTCTGCTCTCGAGGCGCTGAGTGGCTGTGCGCACCAAGCATTTCTGCT

SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
Query Match 98.2%; Score 3933; DB 7; Length 4015;
Best local Similarity 99.1%; Bred No. 0.

Db 1 GCAGCGTGCCTCCTGCTGGCA CGTGGGAAGCCCTGGCCCCGGGCACCCCCG

Db 61 GCGGCTCCCGCTGCCAGCGTCGCTCCCTGCTGGCGACCACTA CCGCG

QY 128 GCCGCTGGCCACGTTCTGTGGGGCGCCTGGGGCCCCCAGGGCTGGCGGCTGGTGC.

Db	121	GC CGT TGG CCA GGT TCG TCG CGG CCT GGG GCG CCA GGG CTT GCG GCG TGG TGC
Qy	188	GG ACC CGG CGG GTT TCC CGG CGC TGT TGG CCG CCA GTT GCT TGG TGT TGG TGG CCG TT

Db 181 GGACCGGGGCTTTCCGGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTT

QY
248 ACGGCGGCCCGCCGGCCCCCTCCTTCGGCAAGGTGTCTGCCTGAAGGAGC

Db 241 ACGGCGCCCCCGCGCGCCCCCTCTTCGGCAAGGTGTCTGTGCTGAAGGAGC

DB
241 ACGGCGCCCCCCCCGCCGGCCCTCCTTCGGCCAGGTGTCTGCCTGAAGGAC

QY 308 CCGAGTGTGCAGAGGCTGTCCAGCGCGGCGGAGAACGTGCTGGCCCTTCG

Dbb 301 CCGAGTGTGCAGAGGCTGTGCCAGCGCGGCGCGAAGAA CGTGTGGCGCTTGG

CTGTGACAGGGGCCCCGGGGCCCCCGAGGCTTACACACAGCGTGGCAGCTA 427
CTGTGACAGGGGCCCCGGGGCCCCCGAGGCTTACACACAGCGTGGCAGCTA 420
CTGCCAACAGCGTACCGACACTCGGGGGAGCGGGGCTGGGCTGCTGCTGG 487
CTGCCAACAGCGTACCGACACTCGGGGGAGCGGGGCTGGGCTGCTGCTGG 480
CGGTGGGCGACAGCGTGGTTCACCTGTGGCAGCGTGGGCTTGTGCTGGT 547
CGGTGGGCGACAGCGTGGTTCACCTGTGGCAGCGTGGGCTTGTGCTGGT 540
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GCTCCAGCTGGCTTACAGAGTGTGGGCGCGCGTGTACAGCTGGCGCTGGCAC 600
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TGGAACCATAGCGTCAGGAGGCGGGGCTCCCTGGGCGCTGCCAGCCCCGGGTGGAG 720
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AGGCGGGGGGAGTGCAGCGGAGCTGTGGCGTGGCCAGAGGCGCCAGCGTGGCGC 780
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GCCCTGAGCGGAGCGGACCGCGTGGGCGGGGCTCTGGGCGCCACCGGGCAGGAC 840
CGTGGACCGAGTACCGTGGTTCCTGTGGTGTCACTGCGCAGACCGCGCGGAGAGC 907
CGTGGACCGAGTACCGTGGTTCCTGTGGTGTCACTGCGCAGACCGCGCGGAGAGC 900
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ACCTCTTGGAGGTGGCTCTGCGCAGCGGCGACTCCACCGCTGGGCGCGCA 960
CACCAGCGGGCCCCCATCCATCGCGCCACAGCTCCCTGGGACAGCGCTTGTCC 1027
CACCAGCGGGCCCCCATCCATCGCGCCACAGCTCCCTGGGACAGCGCTTGTCC 1020
CGGTGTACGCGGAGACAAGCACTTCTTACTCTTACGCGCAAGGAGCAGCTGCG 1087
CGGTGTACGCGGAGACAAGCACTTCTTACTCTTACGCGCAAGGAGCAGCTGCG 1080
CCCTCTTCTACTCAGCTCTGAGGCGCAGCGTGGCTGGGCTGGGAGCTGGTGA 1147
CCCTCTTCTACTCAGCTCTGAGGCGCAGCGTGGCTGGGCTGGGAGCTGGTGA 1140
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CCCAGCGCTACTGCGAAATGCGGCGCTGTTCTGGAGCTGCTTGGGAAACGACGCA 1267
CCCAGCGCTACTGCGAAATGCGGCGCTGTTCTGGAGCTGCTTGGGAAACGACGCA 1260
TGCCCTTACGGGGTCTCTCAAGACGACTGCCCGCTGGGAGCTGGGCTCACCCCAGC 1327
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ACAGACCCCGCTGCGTGGTGGTGTGCTGCGCAGACAGCGCCCTGGCAGGTGTA 1447
ACAGACCCCGCTGCGTGGTGGTGTGCTGCGCAGACAGCGCCCTGGCAGGTGTA 1440
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1441 CGGCTTGTGGCGGCTGCTGCTGCGCGGCTGCTGCGCGGCTGCTGCGCGGCT 1440
1508 CAACGAAACCGCGCTTCTCAGGACACCAAGAGTTCATCTCCCTGGGAGAC 1507
1501 CAACGAAACCGCGCTTCTCAGGAAACCAAGAGTTCATCTCCCTGGGAGAC 1500
1568 GCTCTGCTGCGAGGCTGACGCTGAAAGATGAGCGTGGGAGCTGCGCTTGGC 1567
1561 GCTCTGCTGCGAGGCTGACGCTGAAAGATGAGCGTGGGAGCTGCGCTTGGC 1560
1528 GAGCCCAAGGGTGTGCTGCTGCTGCGCGCAGAGCAAGCTGCTGCTGAGGAGA 1527
1521 GAGCCCAAGGGTGTGCTGCTGCTGCGCGCAGAGCAAGCTGCTGCTGAGGAGA 1520
1588 CAAGTCTCTGCACTGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1587
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1868 GGAAGCAGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1867
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1928 CTTCAATCCCAAGCTGACGCGGCTGCGGCGGATTTGTAACAATGAGTACGTCG 1927
1921 CTTCAATCCCAAGCTGACGCGGCTGCGGCGGATTTGTAACAATGAGTACGTCG 1920
1988 CAGAAAGTTCGCGAGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1987
1981 CAGAAAGTTCGCGAGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
2048 CAGCGCTCTCAACTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2047
2041 CAGCGTCTCTCAACTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
2108 CTTGGAAGATATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2107
2101 CTTGGAAGATATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
2168 GCCGCTGAGCTGTA-----CA 2167
2161 GCCGCTGAGCTGTA-----CA 2160
2192 GGAAGGCTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAG 2191
2221 GGAAGGCTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAG 2220
2252 TCGTATGCGGTGTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2251
2281 TCGTATGCGGTGTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280
2312 CGTCTTACCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2311
2341 CGTCTTACCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340
2372 GACGAGCGCTGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAG 2371
2401 GACGAGCGCTGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAG 2400
2432 CAGTGGCTCTTGAAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAG 2431
2461 CAGTGGCTCTTGAAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAG 2460
2492 CAGTCTTACTGTCAGTGGCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAG 2491

Qy	3632	GAGTGTCCAGCACACCTGGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTC
Db	3661	GAGTGTCCAGCACACCTGGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTC
Qy	3692	GGGCGAGCTTTTCTCATCCAGGAGCCGGCTTCCACTCCCCACATAGGAATAG
Db	3721	GGGCGAGCTTTTCTCATCCAGGAGCCGGCTTCCACTCCCCACATAGGAATAG
Qy	3752	CGAGATCGGCATGTTCACGCCCTGGCCCTGCCCTCTTTGGCTTCCACCCCC
Db	3781	CCGATTCGGCATTTTTCACCCCTGGCCCTGCCCTCTTTGGCTTCCACCCCC
Qy	3812	AGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAAATTGGAGTGACCAA
Db	3841	AGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAAATTGGAGTGACCAA
Qy	3872	CCCTGTATACAGGCGAGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAA
Db	3901	CCCTGTATACAGGCGGAGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAA
Qy	3932	GAGTGCTGTGGGAGTAAAAATATCGAATATATGAGTTTTTTTCAGTTTTTGAAAAA
Db	3961	GAGTGCTGTGGGAGTAAAAATCTCGAATATATGAGTTTTTTTCAGTTTTTGAAAAA

RESULT 14
ACC44482
ID ACC44482 standard; DNA; 4015 BP.

XX	ACC44482;	
XX	AC	
XX	XX	
XX	DT	29-AUG-2003 (first entry)
XX	XX	
XX	DE	Human telomerase reverse transcriptase gene.
XX	DE	
XX	KW	Gene; ds; human; telomerase reverse transcriptase; adipogenic
XX	KW	primary preadipocyte cell; adipogenesis; obesity; adipocytokine
XX	KW	anorectic; adiponectin; insulin.
XX	XX	
XX	OS	Homo sapiens.
XX	XX	
XX	Key	Location/Qualifiers
XX	CDS	56..3454
XX	FT	/*tag= a
XX	FT	/product= "telomerase reverse transcriptase"
XX	XX	
XX	PN	WO2003031640-A2.
XX	XX	
XX	PD	17-APR-2003.
XX	XX	
XX	PP	07-OCT-2002; 2002WO-US031635.
XX	XX	
XX	PR	06-OCT-2001; 2001US-0327650P.
XX	PR	08-OCT-2001; 2001US-0327651P.
XX	XX	
XX	PA	(BOST-) BOSTON MEDICAL CENT. CORP.
XX	XX	
XX	PI	Kirkland J, Tchkonja T;
XX	XX	
XX	DR	WPI; 2003-421278/39.
XX	DR	P-PSDB; ABR56045.
XX	XX	
XX	PT	New primary preadipocyte strain expressing telomerase reverse
XX	PT	transcriptase, useful in research applications, screening assa
XX	PT	clinical applications, and in the administration of therapeutic
XX	PT	particularly for obesity.
XX	XX	
XX	PS	Disclosure; Page 11-13; 53pp; English.
XX	XX	
XX	CC	The invention relates to the generation of primary preadipocyte
XX	CC	strains that express telomerase reverse transcriptase (TERT-1
XX	CC	cataltic subunit of telomerase), and maintain and/or enhance

and maintain adipogenic capacity of the cell. This sequence
the gene encoding the TRP protein. The cell strain can be
search to study all aspect of adipogenesis, especially in
> researching treatments for e.g. obesity. The cell can also be
enify adipogenesis modulators for use as therapeutic agents
mones, growth factors, cytokines, enzymes, cholesterol binding
cholesterol removing proteins or their combinations.
ly, the therapeutic agent may be an adipocytokine, preferably
1, or insulin

15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
 milarity 98.2%; Score 3933; DB 7; Length 4015;
 nilarity 99.1%; P-red. No. 0;
 Conservative 0; Mismatches 0; Indels 36; Gaps 1;
 1AGGGCTGGCTCTGCTGCGACAGTGGGAAGCCCTGGGCCCCGGCCACCCCCCGCATGCC 67
 2AGGGCTGGCTCTGCTGCGACAGTGGGAAGCCCTGGGCCCCGGCCACCCCCCGCATGCC 60
 3GGCTCCCGCTCCCGAGCGGTGGCTCCCTGCTGCCAGCCACTACCGCAGGTGCT 127
 4GGCTCCCGCTCCCGAGCGGTGGCTCCCTGCTGCCAGCCACTACCGCAGGTGCT 120
 5CGTGGCCACAGTTCTGTCGGCGCCCTGGGGGCCCCAGGGCTGGCGGTGGTGCAGGCGG 187
 6CGTGGCCACAGTTCTGTCGGCGCCCTGGGGGCCCCAGGGCTGGCGGTGGTGCAGGCGG 180
 7ACCGGGCGGCTTTCGGGGCGCTGGTGGCCCAAGTGCCTGGTGGTGGTGGCCCTGGGACGC 247
 8ACCGGGCGGCTTTCGGGGCGCTGGTGGCCCAAGTGCCTGGTGGTGGTGGCCCTGGGACGC 240
 9GGCGGCCCCCGCGGCCCTCTTCGCGCAGGTGCTCTGCGCTGAAAGAGCTGGTGGC 307
 10GGCGGCCCCCGCGGCCCTCTTCGCGCAGGTGCTCTGCGCTGAAAGAGCTGGTGGC 300
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 12GAGTGTCTGACAGAGCTGTGCGAGCGCGCGCGAAGAACAGTCTGGCTTCGGCTTCGC 360
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 14TGCTGGAACGGGGCCCGCGGGGGCCCCCGAGGCCCTTCAACACAGCGTGGCGAGCTA 420
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 16TGCCCAACACGTTACCGACGCACTGGGGGGGACGGGGGGTGGGGGCTGCTGCTGG 480
 17GGTGGGGCGACAGCTGTGTTCACTGTGGCAGCGCTGGCGCTCTTTGTGCTGCT 547
 18GGTGGGGCGACAGCTGTGTTCACTGTGGCAGCGCTGGCGCTCTTTGTGCTGCT 540
 19CTTCCAGCTGGCGCTACAGAGTGTGGGGCGCGCGCTGTACAGCTCGGCGCTGCCAC 607
 20CTTCCAGCTGGCGCTACAGAGTGTGGGGCGCGCGCTGTACAGCTCGGCGCTGCCAC 600
 21AGCGCGGGCCCCCGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGGCAACGGGC 667
 22AGCGCGGGCCCCCGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGGCAACGGGC 660
 23GAAACCATAGCGTCAGGGAGCGCGGGTCCCCCTGGGCCCTGGCAGCCCGGGTGGAG 720
 24GAAACCATAGCGTCAGGGAGCGCGGGTCCCCCTGGGCCCTGGCAGCCCGGGTGGAG 727
 25GGCGGGGGGCGAGTGCAGCGGAAGTCTGCGGTTGCCCAAGAGGCCACAGCGTGGCGC 787
 26GGCGGGGGGCGAGTGCAGCGGAAGTCTGCGGTTGGCCAAAGAGGCCACAGCGTGGCGC 780
 27CCCTTGAGCGGAGCGGACGCCCGTTGGGACGGGTCCTGGGCCACACCGGGCAGGAC 847
 28CCCTTGAGCGGAGCGGACGCCCGTTGGGACGGGTCCTGGGCCACACCGGGCAGGAC 840
 29TGGAACCGGAGTGACCGTGGTTTTCTGTGTGGTGTCACTGTGCCACAGCCCGCGCAAGAC 907

Db	841	CGCTGGACCGAGTACCGGTGTTTCTGTGTGGTGTCACTTGTGCGCAGACCCGCGCG
Qy	908	CACCTCTTTGGAGGTCGGTCTCTGSCACGGCCACTCCACCCTACCGCTCGTGG
Db	901	CACCTCTTTGGAGGTCGGTCTCTGSCACGGCCACTCCACCCTACCGCTCGTGG
Qy	968	GCACACGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGC
Db	961	GCACACGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGC
Qy	1028	CCCGGTGTACGCCGAGACCAAGACATTCCTCTACTCTCTCAGGCGCACAGAGAC
Db	1021	CCCGGTGTACGCCGAGACCAAGACATTCCTCTACTCTCTCAGGCGCACAGAGAC
Qy	1088	GCCCTCCTCTACTCTCAGCTCTCTGAGGCCACAGCTGACTGGCGCTCGGAGGC
Db	1081	GCCCTCCTCTCTACTCTCAGCTCTCTGAGGCCACAGCTGACTGGCGCTCGGAGGC
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XX	
DT	17-JAN-2000 (first entry)

merase reverse transcriptase cDNA.

merase reverse transcriptase; hTERT; telomerase; hEST2; protein component; cell proliferative capacity; telomerase; telomerase-related condition; cancer; application; telomerase related condition; cancer; agent; telomerase expression; telomerase activity; d

ns.

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8; 98US-00052919.
RON CORP.
IV TECHNOLOGY CORP.

Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;

610834/52.

polynucleotides for human telomerase reverse transcriptase used
sing or treating cancer.

ig 1; 31pp; English.

t sequence encodes for human telomerase reverse transcriptase is the catalytic protein component of telomerase and is also known as hTERT. This correlates with cell proliferative capacity, tumorigenicity, and the development of a neoplastic phenotype. Human telomerase oligonucleotides are useful for diagnostic or prognostic use in telomerase related conditions, including cancer. They are also used as therapeutic agents, for inhibition of telomerase activity.

015 BP; 663 A; 1364 C; 1274 G; 714 T; 0 U; 0 Other;

98.1%; Score 3931.4; DB 2; Length 4015;

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Mismatches	0	0%
Indels	1	100%
Gaps	0	0%

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CGGGTCCC GGTCGAGCGTGCGTCCCTGCTGGCAGCCACTACCGCGAGGTGCT 120

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Qy	908	CACCTCTTTGGAGGGTGGCTCTCTGGCA CGCGGCACTCCACCGATCCGTG
Db	901	CACCTCTTTGGAGGGTGGCTCTCTGGCA CGCGGCACTCCACCGATCCGTG
Qy	968	GCACACGCGGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGCG
Db	961	GCACACGCGGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGCG
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Db	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCGCCGCTCGAGCTCGCGTCA
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